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Patentanmeldung Nr. Patent application No. Demande de brevet n°

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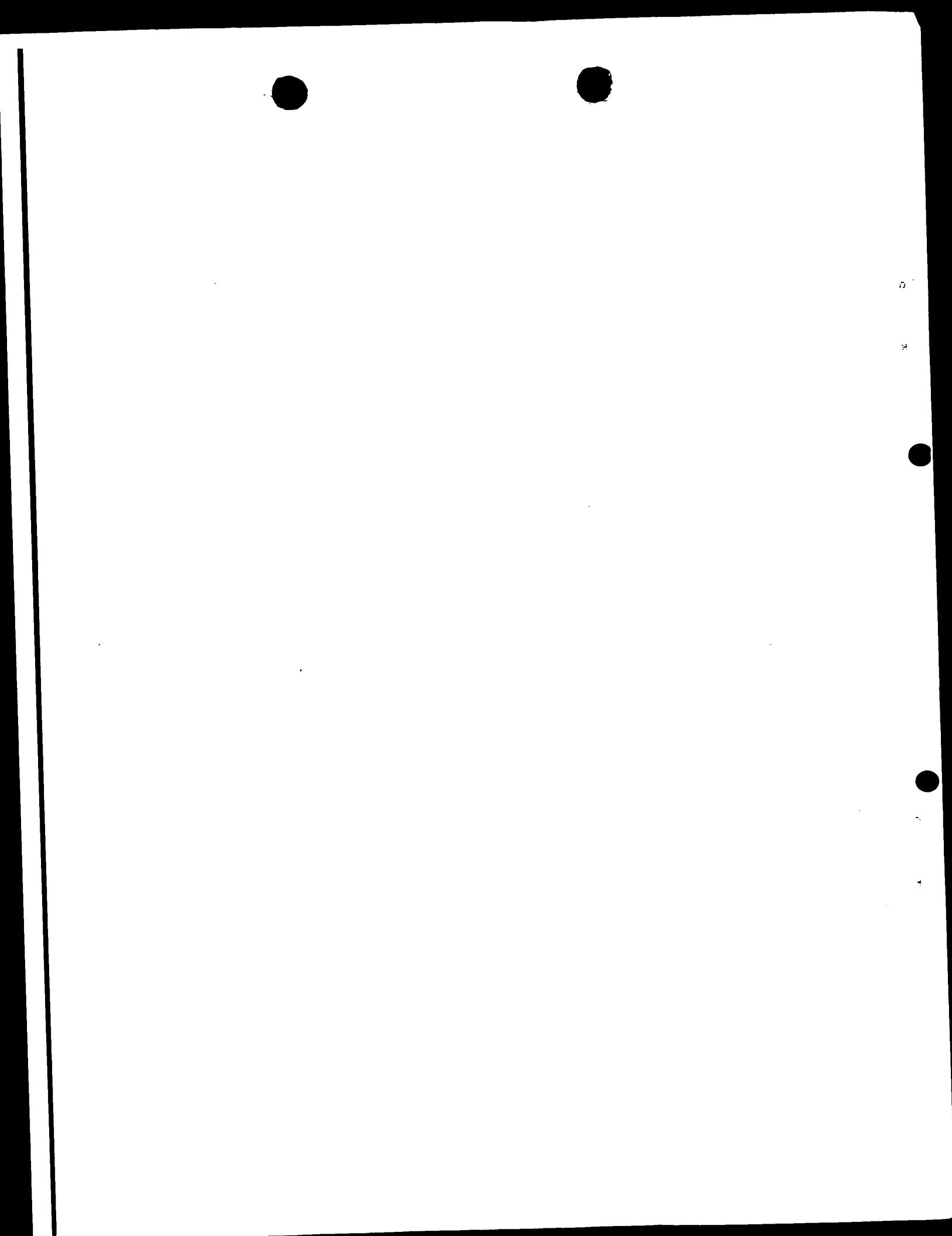
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Chimeric promoters capable of mediating gene expression in plants upon pathogen infection and uses thereof

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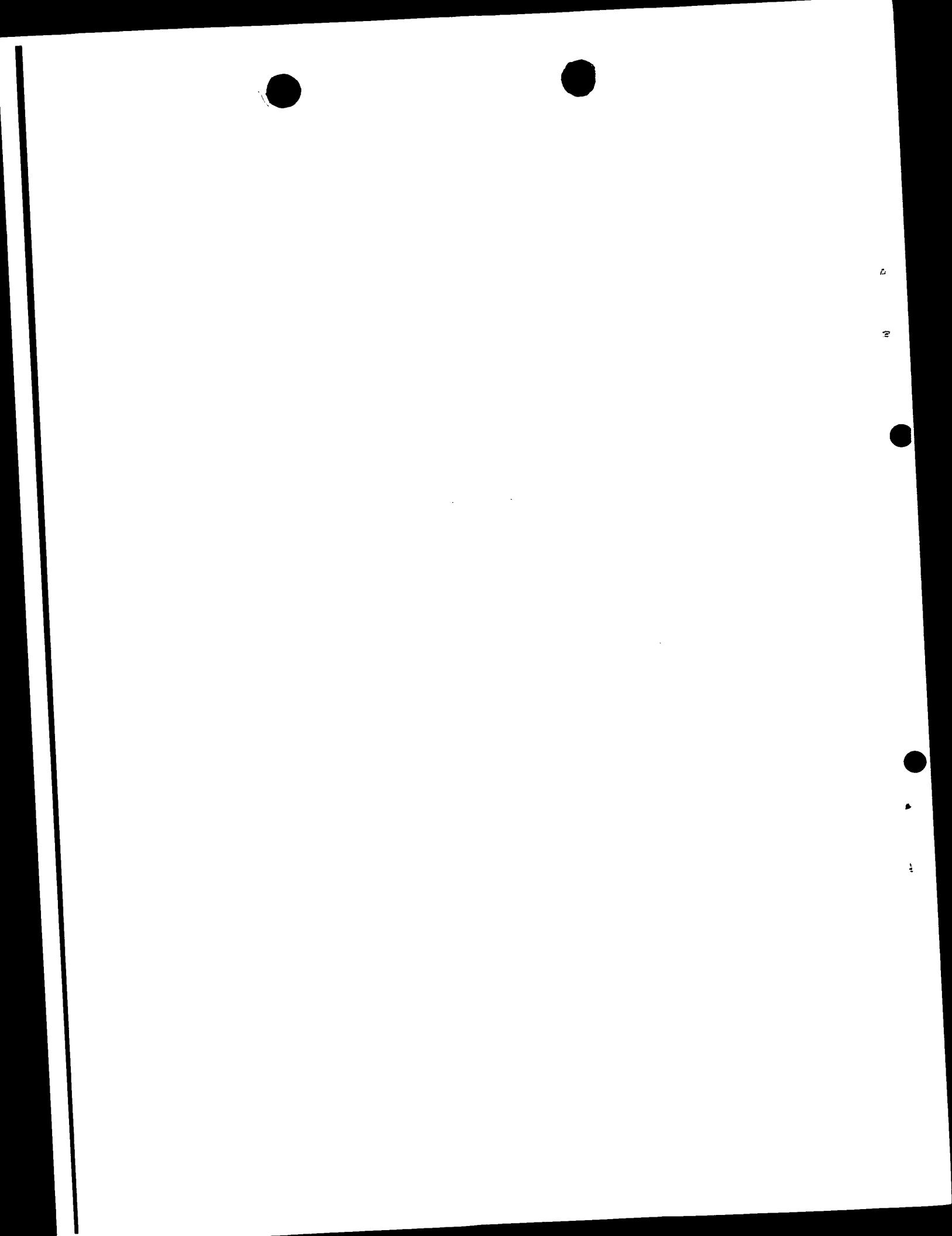
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CHIMERIC PROMOTERS CAPABLE OF MEDIATING GENE EXPRESSION IN PLANTS UPON PATHOGEN INFECTION AND USES THEREOF

The present invention relates to synthetic promoters capable of mediating gene expression in plants upon pathogen infection. The present invention also relates to recombinant genes and vectors comprising said chimeric promoters as well as to host cells transformed with such chimeric promoters, recombinant genes or vectors. The present invention additionally relates to diagnostic compositions and kits comprising such chimeric promoters, recombinant genes, vectors or cells. The present invention also relates to methods for the identification of compounds being capable of activating or inhibiting genes that are specifically expressed in plants upon pathogen infection employing the above described means. Furthermore, the present invention relates to transgenic plant cells, plant tissue and plants containing the above-described chimeric promoters, recombinant genes and vectors as well as to the use of the aforementioned chimeric promoters, recombinant genes, vectors and/or compounds identified by the method of the invention in plant cell and tissue culture, plant breeding and/or agriculture.

The engineering of disease resistance in crops is a major focus of plant biotechnology. One of the most promising approaches to this problem is to engineer defence reactions that are closely related to natural defence mechanisms such as hypersensitive cell death at infection sites, where the cells immediately surrounding an infection site die in order to prevent further spread of the pathogen (Strittmatter, Bio/Technology 13 (1995), 1085-1089). The controlled generation of highly localised necrotic lesions depends, however, on restricting any cytotoxic activity to the infection sites. This therefore requires promoters that are rapidly and locally

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responsive to pathogen attack but that also show negligible activity in uninfected tissues.

Initial attempts using large promoter fragments from pathogenesis-related genes such as *prp1-1* have suffered from the disadvantage that it is difficult to isolate a promoter that is totally pathogen specific with substantially no activity in non-infected tissue (Strittmatter, 1995). It seems likely therefore that very few, if any, naturally occurring promoters will be suitable for this purpose.

Recent advances in the detailed study of defence related genes have identified a number of functionally defined *cis*-acting regulatory DNA elements within pathogen inducible promoters (Korfhage, The Plant Cell 6 (1994), 695-708, Raventos, Plant J. 7 (1995), 147-155, Rushton, EMBO J. 15 (1996), 5690-5700). A number of *cis*-acting elements that are necessary for the response to pathogens have been defined. These include Boxes P and L from the parsley PAL genes (Logemann, Proc. Natl. Acad. Sci. USA 92 (1995), 5905-5909), Boxes H and G from soybean PAL and 4CL (Loake, Proc. Natl. Acad. Sci. USA 89 (1992), 9230-9234), together with a number of less well defined elements. However, while it was shown for a number of such *cis*-acting elements that they are necessary for elicitor inducibility it was not known whether these elements are sufficient to direct pathogen-induced expression in plant cells and planta on their own. Recently, it has only been shown for the Box W1 from parsley (Rushton, EMBO J. 15 (1996), 5690-5700) and ERE from the maize *Prms* (Raventos, Plant J. 7 (1995), 147-155) that four copies of these elements alone are sufficient to direct elicitor responsive expression to some extent in transient gene expression assays. However, inducibility and background level of expression of the constructs investigated in Rushton, 1996 and Raventos, 1995 greatly varied and at best an about 10-fold induction of reporter gene expression was observed that may not be sufficient to supply the above-described biotechnological needs. Accordingly, it was unclear whether these or any other *cis*-acting elements may be useful to specifically suppress or confer local gene expression in plants upon pathogen infection.

Thus, the technical problem of the present invention is to provide promoters that are rapidly and locally responsive to pathogen attack but show negligible activity in uninfected parts of the plant and that can be used for engineering of disease resistant crops.

The solution to this technical problem is achieved by providing the embodiments characterized in the claims.

Accordingly, the invention relates to a chimeric promoter capable of mediating local gene expression in plants upon pathogen infection comprising

- (i) at least one cis-acting element sufficient to direct elicitor-specific expression comprising the nucleotide sequence of any one of SEQ ID NOS: 3 to 14, and
- (ii) a minimal promoter.

The term "capable of mediating local gene expression in plants upon pathogen infection" as used herein means that said promoter is capable of controlling the expression of a heterologous DNA sequence at infection sites, analogous or closely related to the controlled expression of pathogen related genes which are involved in the natural resistance in most incompatible host/pathogen interactions, such as the hypersensitive cell death at infection sites of a part of a plant. Thus, the chimeric promoter of the invention is characterized by its capability of mediating localized transcriptional activation selectively in response to pathogen attack or in response to stimuli that mimic pathogen attack such as elicitors prepared from, e.g., pathogens such as fungi or bacteria or derivatives thereof. The transcriptional activation by the chimeric promoter of the invention may also occur in cells surrounding the actual infection site due to cell-cell interactions. The chimeric promoter of the invention may advantageously not or only to a small extent be inducible upon other stimuli such as abiotic stress. Preferably, the induction from the chimeric promoter upon pathogen attack or elicitor treatment is at least about 10-fold higher, preferably 20-fold higher and particularly 30-fold higher than its activation, if any, by abiotic stress.

However, the expression specificity conferred by the chimeric promoters of the invention may not be limited to local gene expression due to pathogens, for example, they may be combined with further regulatory sequences that provide for tissue specific gene expression. The particular expression pattern may also depend on the plant/vector system employed. However, expression of heterologous DNA sequences driven by the chimeric promoters of the invention predominantly occurs upon pathon infection or treatment with a corresponding elicitor unless certain elements of the invention were taken and designed by the person skilled in the art to control the expression of a heterologous DNA sequence certain cell types.

The term "cis-acting element sufficient to direct elicitor-specific expression" denotes a short stretch of a DNA preferably between 6 and 35 nucleotides in length that when combined with a minimal promoter such as the CaMV 35S minimal promoter (positions -46 to +8) is capable of directing high level elicitor-specific expression of a heterologous DNA sequence. Preferably, said elicitor is fungal elicitor that can be prepared by conventional means; see, e.g., Ayers, Plant Physiol. 57 (1976), 760-765; Grosskopf, J. Plant Physiol. 138 (1991), 741-746; Kombrink, Plant Physiol. 81 (1986), 216-221; West, Naturwissenschaften 68 (1981), 447-457.

The term "minimal promoter", within the meaning of the present invention refers to nucleotide sequences necessary for transcription initiation, i.e. RNA polymerase binding, and may also include, for example, the TATA box.

The term "pathogen" includes, for example, bacteria, viruses, fungi and protozoa as well as elicitors prepared therefrom.

In accordance with the present invention a number of cis-acting elements have been identified that alone are sufficient to direct high level fungal elicitor-specific expression and that can be used to construct novel synthetic promoters that for the first time meet the requirements for engineering disease resistant crops.

Studies that have been performed in accordance with the present invention employed a homologous transient expression system that uses parsley (*Petroselinum crispum*) protoplasts derived from cultured cells. This system is one of very few where the protoplasts respond to fungal elicitor molecules in an almost identical way to cells in the intact plant (Dangl, EMBO J. 6 (1987), 2551-2556; Hahlbrock, Proc. Natl. Acad. Sci. USA 92 (1995), 4150-4157). This allows the study of elicitor-responsive *cis*-acting elements, something that is difficult in many other experimental systems.

Eleven *cis*-acting elicitor-responsive elements (SEQ ID NOS: 3 to 13) were identified in accordance with the present invention. Monomers and multimers of each element were constructed in addition to synthetic promoters consisting of two or more of these elements in combination. Each construct was synthesised with either BamHI ends or with a Spel site at the 5' end and an XbaI site at the 3' end and then cloned into the corresponding restriction site in front of a minimal CaMV 35S promoter (-46 to +8) in the vector MS23-pBT10-GUS (Sprenger, Ph.D. thesis, University of Köln, Köln, Germany (1997); see Figure 1 (SEQ ID NO: 15) and Figure 2). The distance between the insertion site and the TATA Box varied between 25 and 70bp depending on the insertion site employed and only slight differences, if any, were seen when the same element was inserted into different restriction sites.

The experiments performed in accordance with the present invention demonstrate that the *cis*-acting elements direct pathogen-induced expression *in vivo*, being active as monomers, multimers and in combination with each other within synthetic promoters. They therefore meet the biotechnological requirements for the engineering of disease resistance.

In accordance with the present invention these novel chimeric promoters cloned in front of the GUS coding region and the resulting chimeric genes were introduced by means of vacuum infiltration mediated gene transfer into *Arabidopsis* plants; see Example 6. The expression pattern observed in the transgenic plants containing the GUS marker gene under the control of the chimeric promoter of the invention

revealed expression in tissue infected by *Pseudomonas syringae* and in some cases also local expression in wounded tissues.

The chimeric promoter of the invention may be preferably comprised only of the above defined cis-acting elements and a minimal promoter. As will be discussed below, other regulatory sequences may be added or present dependent on the intended use of the chimeric promoter of the invention. However, preferably the chimeric promoter of the invention lacks elements that interfere with the elicitor specific expression and/or which are responsible for the non-selective expression of the promoter the cis-acting element of the invention was derived from.

To obtain possible expression in all tissues of a transgenic plant, the minimal regulatory sequences of constitutive promoters are often used, such as the 35 S promoter of CaMV (Odell, Nature 313 (1985), 810-812) or promoters of the polyubiquitin genes of maize (Christensen, Plant Mol. Biol. 18 (1982), 675-689). It is also immediately evident to the person skilled in the art that further regulatory elements may be added to the chimeric sequences of the invention. For example, transcriptional enhancers and/or sequences which allow for further induced expression of the chimeric promoter of the invention may be employed. Enhancer sequences functional in plants include, for example, ocs-element (Ellis, EMBO J. 6 (1987), 3203-3208); the family of ACGT-elements (hex-motif, G-box as 1-element) (Williams, Plant Cell 4 (1992), 485-496) and the cyt-1 element (Neuteboom, Plant J. 4 (1993), 525-534). In order to achieve expression in specific tissues of a transgenic plant it is possible to use tissue specific promoters (see, e.g., Stockhaus, EMBO J. 8 (1989), 2245-2251). Known are also promoters which are specifically active in tubers of potatoes or in seeds of different plants species, such as maize, Vicia, wheat, barley etc. Furthermore, the chemically inducible Tet-system may be employed (Gatz, Mol. Gen. Genet. 227 (1991); 229-237). Further suitable promoters are known to the person skilled in the art and are described, e.g., in Ward (Plant Mol. Biol. 22 (1993), 361-366).

Preferably, the chimeric promoter of the invention further comprises a cis-acting element having the nucleotide sequence of SEQ ID NO: 1 or 2; see Example 5.

In a particularly preferred embodiment of the invention the chimeric promoter comprises homo- and/or hetero-multimeric forms of said cis-acting element(s); see also the appended Example 5. Preferably, said multimeric form is a dimer or tetramer. Particular preferred are those combinations of cis-acting elements that are described in Example 5 and which combination provide for an at least 20-fold, preferably at least 30-fold and particularly preferred at least about 50-fold induction.

In a preferred embodiment of the chimeric promoter of the invention the minimal promoter is derived from the CaMV35S promoter, CHS promoter, PR1 promoter, or hcbt2 promoter. However, other minimal promoters from other sources may be employed as well.

In a further preferred embodiment of the chimeric promoter of the invention, the distance between said cis-acting element and said minimal promoter is 25 to 70 base pairs. In addition or alternatively, a spacer region preferably composed of 4 to 10 base pairs separates at least two of said cis-acting elements in the chimeric promoter. Likewise, it is preferred that at least two of said multimeric forms in the chimeric promoter described above are separated by a spacer of between about 50 to 1000 base pairs.

In a particularly preferred embodiment of the chimeric promoter of the invention the induction of gene expression upon elicitor treatment or pathogen infection is at least 15-fold. As discussed before, the cis-acting elements so far investigated in the prior art only provided for induction upon elicitor treatment of about 10-fold. However, a 10-fold induction of a recombinant gene encoding, e.g., an anti-viral protein may not be sufficient to rapidly and efficiently combat against the pathogen. The present invention provides several cis-acting elements that are capable of inducing high level expression of a given DNA sequence up to 400-fold induction; see, e.g., Example 1.

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Furthermore, the invention demonstrates that the combination of otherwise weak cis-acting elements can provide for a substantial increase of the overall inducibility of the chimeric promoter; see Example 5. Thus, the present invention for the first time provides a generally applicable method for how to construct and use chimeric promoters in the field of plant biotechnology. As will be noted from the appended Examples, the background value of the chimeric promoters of the invention may vary to a certain extent. The person skilled in the art therefore may employ different chimeric promoters with different background levels and inducibility depending on the intended use. For example, if the approach of coat protein-mediated protection against virus infection is used the chimeric promoter employed may have high background level expression that would not harm the plant and which upon viral infection would increase at high levels such that resistance to the virus can be obtained. The same rational would apply to, e.g., an antisense or ribozyme mediated protection or the engineering of resistance to fungal pathogens by the expression of anti-fungal proteins etc. On the other hand, where the generation of race-specific resistant genes and artificial generation of hypersensitive cell death is intended, preferably a chimeric promoter is used that has low or substantially no background activity and that only upon pathogen attack is activated to an extent that sufficient level of toxic protein is made so as to cause the cell to die. The selection of the appropriate chimeric promoter of the invention depending on its use is well within the skill of the person skilled in the art.

Examples of the different possible applications of the chimeric promoter according to the invention as well as its cis-acting elements will be described in detail in the following.

Hence, in a further embodiment, the present invention relates to a recombinant gene comprising the above-described chimeric promoter. Preferably, the recombinant gene is configured such that the chimeric promoter is operatively linked to a heterologous DNA sequence.

The term "heterologous" with respect to the DNA sequence being operatively linked to the chimeric promoter of the invention means that said DNA sequence is not naturally linked to the chimeric promoter of the invention.

The term "operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. The chimeric promoter "operably linked" to a heterologous DNA sequence is ligated in such a way that expression of a coding sequence is achieved under conditions compatible with the control sequences. Expression comprises transcription of the heterologous DNA sequence preferably into a translatable mRNA. Regulatory elements ensuring expression in eukaryotic, i.e. plant cells are well known to those skilled in the art. In the case of eukaryotic cells they comprise optionally poly-A signals ensuring termination of transcription and stabilization of the transcript, for example, those of the 35S RNA from Cauliflower Mosaic Virus (CaMV) and the Nopaline Synthase gene from Agrobacterium tumefaciens. Additional regulatory elements may include transcriptional as well as translational enhancers. A plant translational enhancer often used is the CAMV omega sequences, the inclusion of an intron (Intron-1 from the Shrunken gene of maize, for example) has been shown to increase expression levels by up to 100-fold. (Mait, Transgenic Research 6 (1997), 143-156; Ni, Plant Journal 7 (1995), 661-676). In this respect, it should be noted that in one embodiment of the recombinant gene of the invention at least one of said cis-acting elements is located in the 5'- or 3'-untranslated region or in an intron of the recombinant gene.

In a preferred embodiment of the recombinant gene of the invention said heterologous DNA sequence encodes a (poly)peptide, cytotoxic protein, antibody, antisense RNA, sense RNA, ribozyme or transcription factor.

The recombinant gene of the invention can be used alone or as part of a vector to express heterologous DNA sequences, which, e.g., encode proteins for, e.g., the control of disease resistance or diagnostics of pathogen inducible or related gene

expression. The recombinant gene or vector containing the DNA sequence encoding an RNA or a protein of interest is introduced into the cells which in turn produce the RNA or protein of interest. For example, the chimeric promoter of the invention can be operatively linked to DNA sequences encoding Barnase for use in the production of localized cell death in plants upon pathogen attack.

On the other hand, said protein can be a scorable marker, e.g., luciferase, green fluorescent protein or β -galactosidase. This embodiment is particularly useful for simple and rapid screening methods for compounds and substances described herein below capable of modulating pathogene specific or elicitor inducible gene expression. For example, transgenic plant cells can be cultured in the presence and absence of a candidate compound in order to determine whether the compound affects the expression of genes which are under the control of chimeric promoters of the invention, which can be measured, e.g., by monitoring the expression of the above-mentioned marker. It is also immediately evident to those skilled in the art that other marker genes may be employed as well, encoding, for example, a selectable marker which provides for the direct selection of compounds which induce or inhibit the expression of said marker.

The chimeric promoters of the invention may also be used in methods of antisense approaches. The antisense RNA may be a short (generally at least 10, preferably at least 14 nucleotides, and optionally up to 100 or more nucleotides) nucleotide sequence formulated to be complementary to a portion of a specific mRNA sequence and/or DNA sequence of the gene of interest. Standard methods relating to antisense technology have been described; see, e.g., Klann, Plant Physiol. 112 (1996), 1321-1330. Following transcription of the DNA sequence into antisense RNA, the antisense RNA binds to its target sequence within a cell, thereby inhibiting translation of the mRNA and down-regulating expression of the protein encoded by the mRNA.

Furthermore, appropriate ribozymes can be employed (see, e.g., EP-A1 0 291 533, EP-A1 0 321 201, EP-A2 0 360 257) which specifically cleave the (pre)-mRNA of a target gene. Selection of appropriate target sites and corresponding ribozymes can

be done as described for example in Steinecke, Ribozymes, Methods in Cell Biology 50, Galbraith, eds Academic Press, Inc. (1995), 449-460. Further applications of the chimeric promoter are evident to the person skilled in the art and can be derived from the literature, e.g., Strittmatter and Wegener, Zeitschrift für Naturforschung 48c (1993), 673-688; Kahl, J. Microbiol. Biotechnol. 11 (1995), 449-460 and references cited therein.

Said transcription factor can for example be a master regulatory factor that controls the expression of a cascade of genes involved in pathogen defense of the plant (Grotewold, Plant Cell 10 (1998), 721-740; Rushton and Somssich, Curr. Opin. Plant Biol. 1 (1998), 311-315). Alternatively, it can be a hybrid transcription factor containing a DNA-binding domain (e.g. of GAL4 or of the bacteriophage 434) and an activator domain (e.g. of VP16 or of any functional plant activator domain), which, when expressed in transgenic plants containing an antisense target gene under the control of a synthetic promoter containing the appropriate cis-acting element recognizing the hybrid factor, leads to specific repression (knock-out) of the desired endogenous gene function (Wilde, Plant Mol. Biol. 24 (1994), 381-388; Guyer, Genetics 149 (1998), 633-639).

Cytotoxic proteins comprise, for example, plant RIPs (ribosome inactivating proteins; Stripe, Bio/Technology 10 (1992), 405-412), defensins (Broekaert, Plant Physiol. 108 (1995), 1353-1358), Bt toxin, α -amylase inhibitor, T4-lysozyme, avirulence gene products, or enzymes such as glucose oxidase which generate reactive oxygen species (Shah, Trends Biotechnol. 13 (1995), 362-368; Shah, Curr. Opin. Biotech. 8 (1997), 208-214; Beachy, Curr. Opin. Biotech. 8 (1997), 215-220; Cornelissen, Plant Physiol. 101 (1993), 709-712; Estruch, Nucleic Acids Res. 22 (1994), 3983-3989).

It is in principle possible to modify the coding sequence in such a way that the protein is located in any desired compartment of the plant cell. These include the nucleus, endoplasmatic reticulum, the vacuole, the mitochondria, the plastids, the apoplast, the cytoplasm etc. Methods how to carry out this modifications and signal sequences ensuring localization in a desired compartment are well known to the

person skilled in the art. (Görlich, Science 271 (1996), 1513-1518; Hicks, Plant Physiol. 107 (1995), 1055-1058; Rachubinski, Cell 83 (1995), 525-528; Schatz, Science 271 (1996), 1519-1526; Schnell, Cell 83 (1995), 521-524; Verner, Science 241 (1988), 1307-1313; Vitale, BioEssays 14 (1992), 151-160).

The present invention also relates to vectors, particularly plasmids, cosmids, viruses and bacteriophages used conventionally in genetic engineering that comprise a chimeric promoter or a recombinant gene of the invention. Preferably, said vector is a plant expression vector, preferably further comprising a selection marker for plants. For example of suitable selector markers, see supra. Methods which are well known to those skilled in the art can be used to construct recombinant vectors; see, for example, the techniques described in Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y. and Ausubel, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1989). Alternatively, the chimeric promoters and recombinant genes of the invention can be reconstituted into liposomes for delivery to target cells.

Advantageously, the above-described vectors of the invention comprise a selectable and/or scorable marker. Selectable marker genes useful for the selection of transformed plant cells, callus, plant tissue and plants are well known to those skilled in the art and comprise, for example, antimetabolite resistance as the basis of selection for dhfr, which confers resistance to methotrexate (Reiss, Plant Physiol. (Life Sci. Adv.) 13 (1994), 143-149); npt, which confers resistance to the aminoglycosides neomycin, kanamycin and paromycin (Herrera-Estrella, EMBO J. 2 (1983), 987-995) and hygro, which confers resistance to hygromycin (Marsh, Gene 32 (1984), 481-485). Additional selectable genes have been described, namely trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histidol in place of histidine (Hartman, Proc. Natl. Acad. Sci. USA 85 (1988), 8047); mannose-6-phosphate isomerase which allows cells to utilize mannose (WO 94/20627) and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO

(McConlogue, 1987, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.) or deaminase from *Aspergillus terreus* which confers resistance to Blasticidin S (Tamura, Biosci. Biotechnol. Biochem. 59 (1995), 2336-2338).

Useful scorable marker are also known to those skilled in the art and are commercially available. Advantageously, said marker is a gene encoding luciferase (Giacomin, Pl. Sci. 116 (1996), 59-72; Scikantha, J. Bact. 178 (1996), 121), green fluorescent protein (Gerdes, FEBS Lett. 389 (1996), 44-47) or β -glucuronidase (Jefferson, EMBO J. 6 (1987), 3901-3907). This embodiment is particularly useful for simple and rapid screening of cells, tissues and plants containing a vector of the invention.

The present invention furthermore relates to host cells comprising a chimeric promoter, recombinant gene or a vector according to the invention wherein the chimeric promoter is foreign to the host cell.

By "foreign" it is meant that the chimeric promoter is either heterologous with respect to the host cell, this means derived from a cell or organism with a different genomic background, or is homologous with respect to the host cell but located in a different genomic environment than the naturally occurring counterpart of said cis-acting element. This means that, if the cis-acting element is homologous with respect to the host cell, it is not located in its natural location in the genome of said host cell, in particular it is surrounded by different genes. The vector or recombinant gene according to the invention which is present in the host cell may either be integrated into the genome of the host cell or it may be maintained in some form extrachromosomally. In this respect, it is also to be understood that the chimeric promoter or recombinant gene of the invention can be used to restore or create a mutant gene via homologous recombination (Paszkowski (ed.), Homologous Recombination and Gene Silencing in Plants. Kluwer Academic Publishers (1994)). The host cell can be any prokaryotic or eukaryotic cell, such as bacterial, insect, fungal, plant or animal cells. Preferred cells are plant cells.

In a further preferred embodiment, the present invention provides for a method for the production of transgenic plants, plant cells or plant tissue comprising the introduction of a chimeric promoter, recombinant gene or vector of the invention into the genome of said plant, plant cell or plant tissue. For the expression of the heterologous DNA sequence under the control of the chimeric promoter according to the invention in plant cells, further regulatory sequences such as poly A tail may be fused, preferably 3' to the heterologous DNA sequence, see also supra. Further possibilities might be to add Matrix Attachment Sites at the borders of the transgene to act as "delimiters" and insulate against methylation spread from nearby heterochromatic sequences.

Methods for the introduction of foreign genes into plants are also well known in the art. These include, for example, the transformation of plant cells or tissues with T-DNA using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*, the fusion of protoplasts, direct gene transfer (see, e.g., EP-A 164 575), injection, electroporation, vacuum infiltration, biolistic methods like particle bombardment, pollen-mediated transformation, plant RNA virus-mediated transformation, liposome-mediated transformation, transformation using wounded or enzyme-degraded immature embryos, or wounded or enzyme-degraded embryogenic callus and other methods known in the art. The vectors used in the method of the invention may contain further functional elements, for example "left border"- and "right border"-sequences of the T-DNA of *Agrobacterium* which allow stable integration into the plant genome. Furthermore, methods and vectors are known to the person skilled in the art which permit the generation of marker free transgenic plants, i.e. the selectable or scorable marker gene is lost at a certain stage of plant development or plant breeding. This can be achieved by, for example cotransformation (Lyznik, Plant Mol. Biol. 13 (1989), 151-161; Peng, Plant Mol. Biol. 27 (1995), 91-104) and/or by using systems which utilize enzymes capable of promoting homologous recombination in plants (see, e.g., WO97/08331; Bayley, Plant Mol. Biol. 18 (1992), 353-361); Lloyd, Mol. Gen. Genet. 242 (1994), 653-657; Maeser, Mol. Gen. Genet. 230 (1991), 170-176; Onouchi, Nucl. Acids Res. 19 (1991), 6373-6378). Methods for the preparation of appropriate vectors are described by, e.g., Sambrook (Molecular Cloning; A

Laboratory Manual, 2nd Edition (1989), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

Suitable strains of *Agrobacterium tumefaciens* and vectors as well as transformation of Agrobacteria and appropriate growth and selection media are well known to those skilled in the art and are described in the prior art (GV3101 (pMK90RK), Koncz, Mol. Gen. Genet. 204 (1986), 383-396; C58C1 (pGV 3850kan), Deblaere, Nucl. Acid Res. 13 (1985), 4777; Bevan, Nucleic Acid Res. 12(1984), 8711; Koncz, Proc. Natl. Acad. Sci. USA 86 (1989), 8467-8471; Koncz, Plant Mol. Biol. 20 (1992), 963-976; Koncz, Specialized vectors for gene tagging and expression studies. In: Plant Molecular Biology Manual Vol 2, Gelvin and Schilperoort (Eds.), Dordrecht, The Netherlands: Kluwer Academic Publ. (1994), 1-22; EP-A-120 516; Hoekema: The Binary Plant Vector System, Offsetdrukkerij Kanters B.V., Albllasserdam (1985), Chapter V, Fraley, Crit. Rev. Plant. Sci., 4, 1-46; An, EMBO J. 4 (1985), 277-287). Although the use of *Agrobacterium tumefaciens* is preferred in the method of the invention, other *Agrobacterium* strains, such as *Agrobacterium rhizogenes*, may be used, for example if a phenotype conferred by said strain is desired.

Methods for the transformation using biolistic methods are well known to the person skilled in the art; see, e.g., Wan, Plant Physiol. 104 (1994), 37-48; Vasil, Bio/Technology 11 (1993), 1553-1558 and Christou (1996) Trends in Plant Science 1, 423-431. Microinjection can be performed as described in Potrykus and Spangenberg (eds.), Gene Transfer To Plants. Springer Verlag, Berlin, NY (1995).

The transformation of most dicotyledonous plants is possible with the methods described above. But also for the transformation of monocotyledonous plants several successful transformation techniques have been developed. These include the transformation using biolistic methods as, e.g., described above as well as protoplast transformation, electroporation of partially permeabilized cells, introduction of DNA using glass fibers, etc.

The resulting transformed plant cell can then be used to regenerate a transformed plant in a manner known by a skilled person.

Alternatively, a plant cell can be used and modified such that said plant cell expresses an endogenous gene under the control of the chimeric promoter. The introduction of the chimeric promoter of the invention which does not naturally control the expression of a given gene or genomic sequences using, e.g., gene targeting vectors can be done according to standard methods, see *supra* and, e.g., Hayashi, Science 258 (1992), 1350-1353; Fritze and Walden, Gene activation by T-DNA tagging. In *Methods in Molecular biology* 44 (Gartland, K.M.A. and Davey, M.R., eds). Totowa: Human Press (1995), 281-294) or transposon tagging (Chandee, *Physiologia Plantarum* 78 (1990), 105-115).

In general, the plants which can be modified according to the invention can be derived from any desired plant species. They can be monocotyledonous plants or dicotyledonous plants, preferably they belong to plant species of interest in agriculture, wood culture or horticulture interest, such as crop plants (e.g. maize, rice, barley, wheat, rye, oats etc.), potatoes, oil producing plants (e.g. oilseed rape, sunflower, pea nut, soy bean, etc.), cotton, sugar beet, sugar cane, leguminous plants (e.g. beans, peas etc.), wood producing plants, preferably trees, etc.

Thus, the present invention relates also to transgenic plant cells comprising, preferably stably integrated into the genome, a chimeric promoter, a recombinant gene or vector according to the invention or obtainable by the above-described method.

Furthermore, the present invention also relates to transgenic plants and plant tissue comprising the above-described transgenic plant cells or obtainable by the above-described method. These plants may show, for example, increased disease resistance.

In a preferred embodiment of the invention, the transgenic plant upon the presence of the chimeric promoter or the recombinant gene of the invention attained

resistance or improved resistance against a pathogen the corresponding wild-type plant was susceptible to.

The term "resistance" covers the range of protection from a delay to complete inhibition of disease development. Examples for pathogens of importance comprise *Phytophthora infestans*, the causal agent of potato late blight disease, *Phytophthora sojae*, root rot pathogen of soybean, *Peronospora parasitica* (downy mildew), *Magnaporthe grisea*, causal agent of rice blast disease, *Erysiphe* spp (powdery mildew), *Pseudomonas syringae* (agent of bacterial blight), *Erwinia amylovora* (fire blight disease), *Erwinia carotovora* (soft rot), *Botrytis cinerea* (downy mildew of grape), *Rhizoctonia solani* and *Pythium debaryanum* (agents of seedling blight or damping off disease).

In yet another aspect the invention also relates to harvestable parts and to propagation material of the transgenic plants according to the invention which contain transgenic plant cells described above. Harvestable parts can be in principle any useful part of a plant, for example, leaves, stems, fruit, seeds, roots etc. Propagation material includes, for example, seeds, fruits, cuttings, seedlings, tubers, rootstocks etc.

As discussed above, novel cis-acting elements have been identified in accordance with the present invention that are capable of conferring elicitor inducible or pathogen specific gene expression in plant cells and plants. Therefore, the present invention also relates to cis-acting elements as defined above or multimeric forms of any one of those as discussed hereinbefore.

Due to the tight regulation of the chimeric promoters of the invention it is evident that they are particularly suited for the identification of compounds that either specifically interact with these cis-acting elements or that act upstream of the signal transduction pathway that leads to activation of genes the cis-acting elements were derived from.

Thus, the present invention further relates to a method for the identification of an activator or inhibitor of genes specifically expressed in plants upon pathogen infection comprising the steps of:

- (a) providing a plant, plant cell, or plant tissue comprising a recombinant DNA molecule comprising a readout system operatively linked to the chimeric promoter of the invention;
- (b) culturing said plant cell or tissue or maintaining said plant in the presence of a compound or a sample comprising a plurality of compounds under conditions which permit expression of said readout system;
- (c) identifying or verifying a sample and compound, respectively, which leads to suppression or activation and/or enhancement of expression of said readout system in said plant, plant cell, or plant tissue.

For the identification of inhibitors, it is advantageous to include an elicitor or an other activator known to be capable of inducing the activity of promoters that contain the cis-acting elements of the chimeric promoters of the invention in step (b) of the above-described method, and to determine whether the compound to be screened suppresses the induction of the readout system by said elicitor or activator.

The term "read out system" in context with the present invention means a DNA sequence which upon transcription and/or expression in a cell, tissue or organism provides for a scorable and/or selectable phenotype. Such read out systems are well known to those skilled in the art and comprise, for example, recombinant genes and marker genes as described above and in the appended examples.

The term "plurality of compounds" in a method of the invention is to be understood as a plurality of substances which may or may not be identical.

Said compound or plurality of compounds may be comprised in, for example, samples of inorganic or organic molecules or, e.g., cell extracts from, e.g., plants, animals or microorganisms. Furthermore, said compound(s) may be known in the art but hitherto not known to be capable of suppressing or activating pathogen related genes. Suitable set ups for the method of the invention are known to the person

skilled in the art. The plurality of compounds may be, e.g., added to the cell or tissue culture medium or soil, injected into the cell or sprayed onto the plant. If a sample containing a compound or a plurality of compounds is identified in the method of the invention, then it is either possible to isolate the compound from the original sample identified as containing the compound capable of suppressing or activating the chimeric promoter of the invention, or one can further subdivide the original sample, for example, if it consists of a plurality of different compounds, so as to reduce the number of different substances per sample and repeat the method with the subdivisions of the original sample. Depending on the complexity of the samples, the steps described above can be performed several times, preferably until the sample identified according to the method of the invention only comprises a limited number of or only one substance(s). Preferably said sample comprises substances of similar chemical and/or physical properties, and most preferably said substances are identical. Preferably, the compound identified according to the above described method or its analog or derivative is further formulated in a form suitable for the application in plant breeding or plant cell and tissue culture. For example, it can be combined with a agriculturally acceptable carrier known in the art.

The compounds which can be tested and identified according to a method of the invention may be expression libraries, e.g., cDNA expression libraries, peptides, proteins, nucleic acids, antibodies, small organic compounds, hormones, peptidomimetics, PNAs or the like (Milner, *Nature Medicine* 1 (1995), 879-880; Hupp, *Cell* 83 (1995), 237-245; Gibbs, *Cell* 79 (1994), 193-198 and references cited supra). Furthermore, genes encoding a putative regulator of genes controlled by the cis-acting elements of the invention and/or which exert their effects up- or downstream from such genes may be identified using, for example, insertion mutagenesis using, for example, gene targeting vectors known in the art (see, e.g., Hayashi, *Science* 258 (1992), 1350-1353; Fritze and Walden, *Gene activation by T-DNA tagging. In Methods in Molecular biology* 44 (Gartland, K.M.A. and Davey, M.R., eds). Totowa: Human Press (1995), 281-294) or transposon tagging (Chandee, *Physiologia Plantarum* 78 (1990), 105-115).

Said compounds can also be functional derivatives or analogues of known inhibitors or activators. Methods for the preparation of chemical derivatives and analogues are well known to those skilled in the art and are described in, for example, Beilstein, Handbook of Organic Chemistry, Springer edition New York Inc., 175 Fifth Avenue, New York, N.Y. 10010 U.S.A. and Organic Synthesis, Wiley, New York, USA. Furthermore, said derivatives and analogues can be tested for their effects according to methods known in the art or as described in the appended examples. Furthermore, peptidomimetics and/or computer aided design of appropriate derivatives and analogues can be used. The cell or tissue that may be employed in the method of the invention preferably is a plant cell, plant tissue or plant of the invention described in the embodiments hereinbefore.

In an additional embodiment, the characteristics of a given compound may be compared to that of a cell contacted with a compound which is either known to be capable or incapable of suppressing or activating the chimeric promoter of the invention or the promoter the cis-acting element of the chimeric promoter is derived from.

The inhibitor or activator identified by the above-described method may prove useful as a plant protective agent or herbicide or pesticide. Thus, in a further embodiment the invention relates to a compound obtained or identified according to the method of the invention said compound being an activator or an inhibitor of genes specifically induced upon pathogen infection.

Furthermore, identification of *trans*-acting factors which interact with the cis-acting elements of the invention can form the basis for the development of novel agents for modulating conditions associated with plant diseases. Identification of *trans*-acting factors is carried out using standard methods in the art (see, e.g., Sambrook, supra, and Ausubel, supra). To determine whether a protein binds to the cis-acting elements of the invention standard DNA footprinting and/or native gel-shift analyses can be carried out. In order to identify the *trans*-acting factor which binds to the cis-

acting elements of the invention, these elements can be used as an affinity reagent in standard protein purification methods, or as a probe for screening an expression library. Once the *trans*-acting factor is identified, modulation of its binding to the *cis*-acting elements of the invention can be pursued, beginning with, for example, screening for inhibitors of *trans*-acting factor binding.

Activation or repression of genes involved in plant defense reactions could then be achieved in plants by applying of the *trans*-acting factor (or its inhibitor) or the gene encoding it, e.g. in a vector for transgenic plants. In addition, if the active form of the *trans*-acting factor is a dimer, dominant-negative mutants of the *trans*-acting factor could be made in order to inhibit its activity. Furthermore, upon identification of the *trans*-acting factor, further components in the pathway leading to activation (e.g. signal transduction) or repression of pathogenesis related genes then can be identified. Modulation of the activities of these components can then be pursued, in order to develop additional agents and methods for modulating the response of plants upon pathogen attack in plants.

Accordingly, the present invention also relates to a plant protection composition comprising the compound identified and obtained by the above described methods. The plant protection composition can be prepared by employing the above-described method of the invention and synthesizing the compound identified as inhibitor or activator in an amount sufficient for use in agriculture. Thus, the present invention also relates to a method for the preparation of an agricultural plant protection composition comprising the above-described steps of the method of the invention and synthesizing the compound so identified or an analog or derivative thereof.

In the plant protection composition of the invention, the compound identified by the above-described method may be preferentially formulated by conventional means commonly used for the application of, for example, herbicides and pesticides or agents capable of inducing systemic acquired resistance (SAR). For example, certain additives known to those skilled in the art stabilizers or substances which facilitate the uptake by the plant cell, plant tissue or plant may be used, for example,

harpins, elicitors, salicylic acid (SA), benzol(1,2,3)thiadiazole-7-carbothioic acid (BTH), 2,6-dichloro isonicotinic acid (INA), jasmonic acid (JA), methyljasmonate.

In a further embodiment, the present invention relates to an antibody specifically recognizing the compound obtainable by the method of the invention or the cis-acting element described above. The antibodies of the invention can be used to identify and isolate other activators and inhibitors of genes in that are involved in plant defense. These antibodies can be monoclonal antibodies, polyclonal antibodies or synthetic antibodies as well as fragments of antibodies, such as Fab, Fv or scFv fragments etc. Monoclonal antibodies can be prepared, for example, by the techniques as originally described in Köhler and Milstein, Nature 256 (1975), 495, and Galfré, Meth. Enzymol. 73 (1981), 3, which comprise the fusion of mouse myeloma cells to spleen cells derived from immunized mammals. Furthermore, antibodies or fragments thereof to the aforementioned peptides can be obtained by using methods which are described, e.g., in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988.

Furthermore, the present invention relates to a diagnostic composition comprising the chimeric promoter, the recombinant gene, the vector, the compound or the antibody of the invention, and optionally suitable means for detection. Said diagnostic compositions may be used for, e.g., methods for screening activators or inhibitors as described above.

In addition, the present invention relates to a kit comprising the chimeric promoter, the recombinant gene, the vector, the compound or the antibody of the invention. The kit of the invention may contain further ingredients such as selection markers and components for selective media suitable for the generation of transgenic plant cells, plant tissue or plants. Furthermore, the kit may include buffers and substrates for reporter genes that may be present in the recombinant gene or vector of the invention. In addition, the kit of the invention may contain compounds such as elicitors, preferably fungal elicitors that can be used as standards for the expression

assays. The kit of the invention may advantageously be used for carrying out the method of the invention and could be, *inter alia*, employed in a variety of applications referred to herein, e.g., in the diagnostic field or as research tool. The parts of the kit of the invention can be packaged individually in vials or in combination in containers or multicontainer units. Manufacture of the kit follows preferably standard procedures which are known to the person skilled in the art.

The kit or its ingredients according to the invention can be used in plant cell and plant tissue cultures, for example, for any of the above described methods for detecting inhibitors and activators of pathogenesis related genes. The kit of the invention and its ingredients are expected to be very useful in breeding new varieties of, for example, plants which display improved properties such as disease resistance.

It is also immediately evident to the person skilled in the art that the chimeric promoters, recombinant genes and vectors of the present invention can be employed to produce transgenic plants with a desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising (i) insect resistance (Vaek, Plant Cell 5 (1987), 159-169), (ii) virus resistance (Powell, Science 232 (1986), 738-743; Pappu, World Journal of Microbiology & Biotechnology 11 (1995), 426-437; Lawson, Phytopathology 86 (1996), 56 suppl.), (iii) resistance to bacteria, insects and fungi (Duering, Molecular Breeding 2 (1996), 297-305; Strittmatter, Bio/Technology 13 (1995), 1085-1089; Estruch, Nature Biotechnology 15 (1997), 137-141), (iv) inducing and maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695) or may be used as highly inducible production systems of heterologous proteins or biopolymers in plants analogous to inducible systems in bacteria.

The present invention for the first time demonstrates that a number of cis-acting elements that are responsible for inducibility of pathogenesis-related genes can be used either alone or in combination with themselves or with other cis-acting elements to construct chimeric promoters that are capable of mediating highly inducible gene expression in plant cells upon elicitor treatment. It is therefore evident

that cis-acting elements derived, e.g., from pathogen-related promoters other than those specifically described above can be used in accordance with the present invention, for example, chitinase promoters; see, e.g., Kellmann, Plant. Mol. Biol. 30 (1996), 351-358. Appropriate promoters that provide a source for such cis-acting elements can be used and obtained from any plant species, for example, maize, potato, sorghum, millet, coix, barley, wheat and rice. Such promoters are characterized by their inducibility upon pathogen infection.

For example, using cDNA of proteins that are specifically expressed in plants upon pathogen attack as probes, a genomic library consisting of plant genomic DNA cloned into phage or bacterial vectors can be screened by a person skilled in the art. Such a library consists, e.g., of genomic DNA prepared from plant leaf tissue, fractionized in fragments ranging from 5 kb to 50 kb, cloned into the lambda vectors such as Lambda EMBL3 or 4, Lambda ZAP, Lambda DASH or Lambda GEM. Phages hybridizing with the probes can be purified. From the purified phage DNA can be extracted and sequenced. Having isolated the genomic sequences corresponding to the genes encoding the PR proteins, it is possible to fuse heterologous DNA sequences to these promoters or their regulatory sequences via transcriptional or translational fusions according to methods well known to the person skilled in the art. In order to identify the regulatory sequences and specific elements of these genes, 5'-upstream genomic fragments can be cloned in front of marker genes such as luc, gfp or the GUS coding region and the resulting chimeric genes can be introduced by means of Agrobacterium tumefaciens mediated gene transfer into plants or transfected into plant cells or plant tissue for transient expression. The expression pattern observed in the transgenic plants or transfected plant cells containing the marker gene under the control of the isolated regulatory sequences reveal the boundaries of the promoter and its cis-acting elements. The isolation of cis-acting elements having the above defined properties can be done by conventional techniques known in the art, for example, by using DNasel footprinting and loss-and gain-of-function experiments. It is then possible to isolate the corresponding promoter region by conventional techniques and test it for

its expression pattern. For this purpose, it is, for instance, possible to fuse the putative cis-acting element with a minimal promoter to a reporter gene, such as GUS, luciferase or green fluorescent protein (GFP) and assess the expression of the reporter gene in transient expression assays or transgenic plants; see also the appended examples.

Thus, the present invention relates to the use of a cis-acting element sufficient to direct elicitor-specific expression and in particular to the use of the chimeric promoter, the recombinant gene, the vector, the cis-acting element and/or the compound of the present invention for the production of pathogen resistant plants or for identifying and/or producing compounds capable of conferring induced resistance to a pathogen in a plant.

In a still further embodiment, the present invention relates to a method of rendering a gene responsive to pathogens comprising inserting at least one cis-acting element sufficient to direct elicitor-specific expression into the promoter of said gene. As is evident to the person skilled in the art a promoter that displays the capabilities of the chimeric promoter of the invention can also be obtained by introducing the cis-acting element as defined above into a promoter of a gene, preferably in close proximity to the transcription initiation site of the gene.

In another embodiment, the present invention relates to a method for preparing a promoter capable of mediating local gene expression in plants upon pathogen infection comprising operably linking a cis-acting element sufficient to direct elicitor-specific expression to a transcription initiation sequence of a promoter. Preferably, said cis-acting element to be inserted in the above-described methods is a cis-acting element of the present invention or as defined in the foregoing embodiments or a multimeric form thereof as defined hereinabove. As mentioned before, the elicitor responsive cis-acting elements are preferably responsive to fungal elicitor.

In a preferred embodiment of the invention, the above-described methods further comprising deleting non-specific cis-acting elements in the promoter. Introduction of the cis-acting element of the invention into a given promoter per se may not be sufficient to direct the promoter to exclusively mediate local gene expression in plants upon pathogen infection. In this case, preexisting elements that may be responsive, for example, to light, hormones, low temperatures, drought or salt stress may be deleted.

The above described methods give rise to novel chimeric promoters that are at least partially, preferably fully controlled by plant/pathogen interaction.

Accordingly, the present invention also relates to the promoter obtainable by a method as described above. Said promoter can then be employed for the embodiments described hereinabove.

These and other embodiments are disclosed and encompassed by the description and examples of the present invention. Further literature concerning any one of the methods, uses and compounds to be employed in accordance with the present invention may be retrieved from public libraries, using for example electronic devices. For example the public database "Medline" may be utilized which is available on the Internet, for example under <http://www.ncbi.nlm.nih.gov/PubMed/medline.html>. Further databases and addresses, such as <http://www.ncbi.nlm.nih.gov/>, <http://www.infobiogen.fr/>, http://www.fmi.ch/biology/research_tools.html, <http://www.tigr.org/>, are known to the person skilled in the art and can also be obtained using, e.g., <http://www.lycos.com>. An overview of patent information in biotechnology and a survey of relevant sources of patent information useful for retrospective searching and for current awareness is given in Berks, TIBTECH 12 (1994), 352-364.

The present invention is further described by reference to the following non-limiting figures and examples.

The Figures show:

Figure 1 Restriction map of the plasmid ms23 (Sprenger, 1997)

Figure 2 Overview cartoon of the plasmid ms23. The Gus reporter gene and minimal -46 CaMV 35S promoter are shown, as are restriction sites found in the polylinker sequence situated 5' to the minimal promoter. The distances (in base pairs) between the restriction sites are also shown.

Figure 3 Overview cartoon of the plasmid pGPTV. The Gus reporter gene and minimal -46 CaMV 35S promoter are shown as are the Spel and XbaI sites used in making the constructs employed. The *nptII* selection marker is also indicated, as are the left and right T-DNA borders (L and R). The terminators (pA_{nos} and p_{nos}) and promoter driving the *nptII* gene (pAg7) are also shown.

The Examples illustrate the invention:

Experimental setup

1. Recombinant DNA techniques

Unless stated otherwise in the examples, all recombinant DNA techniques are performed according to protocols as described in Sambrook (1989), Molecular Cloning : A Laboratory Manual. Cold Spring Harbor Laboratory Press, NY or in Volumes 1 and 2 of Ausubel (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, jointly published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

2. Transient expression vector

All constructs were cloned between the Spel and Xbal sites in pbt10-GUS (ms23) (Sprenger, 1997). At the 3' end of each construct is an intact Xbal site (6 bp) followed immediately by a minimal CaMV 35S promoter (-46 to +8). The 3' end of all inserts are therefore 28 bp upstream of the CAMV TATA Box and 52 bp upstream of the start of transcription. Multiple copies of the elements are separated by 6 base pairs (TCTAGT) created by the ligation of a Spel sticky end with a Xbal sticky end. The sequence of ms23 as a restriction map and an overview cartoon are provided (Figures 1 and 2).

3. Transgenic plant vector

The vector employed was pGPTV-GUS-kan (Becker, Plant Mol. Biol. 20 (1992), 1195-1197). The polylinker, minimal CaMV 35S promoter and GUS reporter gene are identical to ms23. All spacings and orders of *cis*-elements within the constructs are therefore identical to those in the corresponding transient expression constructs in ms23. A cartoon of pGPTV is provided (Figure 3).

4. Transient transfection and expression assays

The transient transfection and expression assays were essentially carried out as described in Dangl, EMBO J. 6 (1987), 2551-2556; Schulze-Lefert, EMBO J. 8 (1989), 651-656; van de Löcht, EMBO J. 9 (1990), 2945-2950. Briefly, five day old subcultured parsley cells are used for the isolation of protoplasts. Protoplasting is achieved by overnight incubation of the cells in 0.24 M CaCl₂ containing 0.25% (w/v) cellulase and 0.05% (w/v) macerozyme at 24° C. Protoplasts are collected by centrifugation (7 min., 100 g), washed with 0.24 M CaCl₂, and then floated in B5 medium (GIBCO/BRL) containing 0.4 M sucrose and 1 mg/ml 2,4-dichlorophenoxyacetic acid. Protoplasts floating after centrifugation (5 min, 100 g) were harvested, counted and adjusted to 2 x 10⁶/ml.

Supercoiled or linearized plasmid DNA (5 -20 µg) containing the chimeric promoter-reporter(GUS) construct was transferred into the protoplasts using the polyethylene glycol (PEG) method (Krens, Nature 296 (1982), 72-74). Each transformation assay

was split and placed into two 3 ml plates. Elicitor was added to one whereas the other served as a control. Both samples were harvested after 8 hours, frozen in liquid nitrogen, crude protein extracts prepared and GUS activity assayed (Jefferson, Plant Mol. Biol. Rep. 5 (1987), 387-405). Bradford assays (Bio-Rad) were used for protein determination.

5. Generation of transgenic plants

Transgenic plants were generated according to the methods described in Bechtold, Mol. Biol. Genet. 316 (1993), 1194-1199; Grant, Science 269 (1995), 843-846 and Dangl, Science 269 (1995), 843-846. Briefly, the promoter elements were cloned in front of the reporter gene of the binary vector pGPTV-GUS-kan (Becker, Plant Mol. Biol. 20 (1992), 1195-1197) and the constructs introduced into the Agrobacterium strain GV3101 (pMP90; (Koncz and Schell, loc. cit.) containing the pMP90 helper plasmid. 500ml cultures were grown in YEB medium containing kanamycin (50µg/ml), rifampicin (100µg/ml) and gentamycin (25µg/ml). Cells were resuspended in infiltration medium (0.5 x Murashige-Skoog salts; 1 x B5 vitamins; 5.0% sucrose and 0.044 µM benzylaminopurine) and vacuum infiltrated into *Arabidopsis* plants by the method of Grant (1995). T1 seeds were surface-sterilised and transformants were selected on MS medium containing 50µg/ml kanamycin. Primary transformants were transferred to soil and tested for GUS expression during pathogenesis and biotic or abiotic stress.

Example 1: Box S is capable of mediating elicitor induced gene expression

Box S (CAGCCACCAAAGAGGACCCAGAAT; SEQ ID NO: 7) has been shown to be necessary for the elicitor-responsive expression of the parsley *eli* 7 genes (Takamiya-Wik, Ph.D. thesis, University of Köln, Köln, Germany (1995)). Together with the results concerning Box N (see Example 4.3) for the first time the core sequence of this type of element has been defined which appears to be AGCCACCANA. The element is not identical to any known elicitor-responsive element although it is very similar to a number of ethylene response elements that

have the core sequence AGCCGCC (GCC Boxes) (Ohme-Takagi and Shinshi, The Plant Cell 7 (1995), 173-182). In the promoters investigated (*eli7-1*, *eli7-2* and *Prp1*) there is always an A residue rather than a G. What difference this difference in sequence makes is at present unclear and it is not known whether Box S is responsive to ethylene. It has however been shown for the first time that the Box S elements with the sequence AGCCACC are elicitor-responsive elements. The present data also show for the first time that GCC Boxes are also elicitor response elements as well as being ethylene response elements. Box S is a very strong elicitor-responsive element. A monomer of Box S gives 11-fold inducibility and a tetramer up to 560-fold inducibility. This clearly shows Box S to be an extremely promising element for biotechnological purposes.

The sequence of the monomer element used is: 5'-
 actagtCAGCCACCAAGAGGGACCCAGAAATtctaga-3' with the element in upper case letters and the SpeI/XbaI ends in lower case letters. Constructs containing 1, 2, 4 and 8 copies of Box S were constructed and subjected to a transient expression assay as described above. The results were as follows:

	minus elicitor	Plus elicitor	Fold induction
1 x S	168	2058	12
2 x S	118	10781	91
4 x S	187	76904	441
8 x S	781	102211	130

These Box S constructs are novel and have high inducibility. Four copies of Box S appears to be the best with a very low background value (187) a high induced level (76904) and a very high fold induction (441 x, the highest of any of the constructs tested).

Example 2: Box D is capable of mediating elicitor inducible gene expression

Box D (TACAATTCAAACATTGTTCAAACAAGGAACC; SEQ ID NO: 11) is present in the parsley PR2 promoter and has never before been reported to be a *cis*-acting element. Box D was identified by DNaseI footprinting, by loss of function experiments in the context of the PR2 promoter and by gain-of-function experiments with monomers and multimers. Box D is a very strong elicitor-responsive element, a tetramer directing 10-fold elicitor-inducibility combined with a very high level of expression, whilst a dimer is less strong but gives 15-20-fold inducibility. This clearly shows Box D to be a promising element for biotechnological purposes.

The sequence of the element used is: 5'-actagtTACAATTCAAACATTGTTCAAACAAGGAACCTctaga-3' with the element in upper case letters and the SpeI/XbaI ends in lower case letters. Constructs containing 1, 2 and 4 copies of Box D were constructed and subjected to the transient expression assay described above. The results were shown below.

	minus elicitor	Plus elicitor	Fold induction
1 x D	346	4002	11
2 x D	1562	31331	20
4 x D	5519	61552	11

These Box D constructs are novel. Two copies of Box D may be the best with a moderate background value (1562), a high induced level (31331) and a good fold induction (20 x).

Example 3: Box U provides for elicitor inducible gene expression

Box U (ATGAAGTTGAAATTCAATAG; SEQ ID NO: 13) is present in the parsley PR2 promoter and has never before been reported to be a *cis*-acting element. Box U

has been defined by DNaseI footprinting, by loss of function experiments in the context of the PR2 promoter and by gain-of-function experiments with monomers and multimers. Box U is a reasonably strong elicitor-responsive element, a tetramer directing 40-fold elicitor-inducibility.

The sequence of the element used is: 5'-
actagtAGTTGAAATTCAATAAGTTGAAATTCAATAtctaga-3' with the element in
upper case letters and the Spel/XbaI ends in lower case letters.

Constructs containing 2 copies of the above Box U sequence were constructed. The results of a transient expression assay are shown below. These therefore contain 4 copies of the Box U element (AGTTGAAATTCAATA; SEQ ID NO: 12). 1 or 2 copies of Box U are also active.

	minus elicitor	Plus elicitor	Fold induction
4 x U	100	3947	39

These Box U constructs are novel. Box U appears to be a moderately strong pathogen-responsive element with a good fold induction (about 40 x).

Example 4: Some W Boxes are capable of mediating elicitor inducible gene expression

The results obtained in accordance with the present invention clearly show that there are great differences between the different W Boxes that have been tested. Some are very strong (Box W2), some weak (Box W1), some are not active at all on their own (Box W3) and some are present as composite elements together with other cis-acting elements (Box N). The W Boxes also have differences outside of the core

TGAC sequences:

Box W1: TTTGACC (SEQ ID NO: 1)

Box W2: TTCAGCC-N₇-TTGACC (SEQ ID NO: 3)
Box W3: TGAC-N₆-GTCA (SEQ ID NO: 5)
Box N: TTTGACC plus GCCACC (S Box) (SEQ ID NO: 8)
Box W_{Amy}: TTGACC within TGAC-N₆-GTCA palindrome (SEQ ID NO: 6)

4.1 Box W1

Box W1 (CACACTTAATTTGACCGAGTAACATTGCC; SEQ ID NO: 2) has previously been identified as a weak elicitor-responsive *cis*-element in the parsley PR1 promoters and a tetramer has been shown to be sufficient to direct elicitor-responsive expression in the parsley transient expression system (Rushton, 1996). Box W1 contains the W box sequence TTGACC and evidence suggests that these elements are bound by the WRKY class of transcription factors. As W boxes have also been found in the monocots Wild oat (Rushton, 1995) and maize (Raventos, 1995) and WRKY proteins have been found in an increasing number of plant species this suggests that the W box elements may be *cis*-acting elements in all plant species. Box W1 had never before been tested on its own for activity as a monomer or in combination with other elements and it was observed that a monomer directs elicitor-inducible expression (5-fold inducibility) and that Box W1 is also active in combination with other elements (see below).

The current results show Box W1 itself, however, to be a weak element. The sequence of the element used (the monomer) is: 5'-actagtCACACTTAATTTGACCGAGTAACATTGCCtctaga-3' with the element in upper case letters and the Spel/XbaI ends in lower case letters. This construct is slightly different than the construct previously reported (Rushton, 1996) as the element is inserted into the Spel/XbaI sites and not BamHI/BglII. Constructs containing 1, 2 and 4 copies of Box W1 were constructed and subjected to the transient expression assay. The results were as follows.

	minus elicitor	Plus elicitor	Fold induction
1 x W1	362	1495	4.1
2 x W1	299	2433	8.1
4 x W1	56	870	<15

The fold induction with 4 x W1 is similar to the previously reported values (Rushton, 1996). Comparison with values for other elements shows Box W1 to be a weak element.

4.2 Box W2

Box W2 (TTATTCAGCCATCAAAGTTGACCAATAAT; SEQ ID NO: 4) has previously been identified as a *cis*-acting element required for the elicitor responsive expression of parsley PR1 promoters in the transient expression system (Rushton, 1996). However, gain of function has been first demonstrated in accordance with the present invention. Box W2, like Box W1, contains a TTGACC element but the rest of the element is totally different and these other sequences play an important role, as a tetramer of Box W1 is a weak element with about 10-fold elicitor inducibility whereas Box W2 directs levels of expression up to 100 times higher than Box W1 with a 50-fold elicitor inducibility. It is shown for the first time that Box W2 alone, as a monomer or multimer, is a very strong elicitor-responsive element and that it is also active in combination with other elements.

The sequence of the element used (the monomer) is: 5'-actagtTTATTCAGCCATCAAAGTTGACCAATAATtctaga-3' with the element in upper case letters and the Spel/XbaI ends in lower case letters. Constructs containing 1, 2, 4 and 8 copies of Box W2 were constructed and subjected to the transient expression assay. The following results were obtained.

	minus elicitor	Plus elicitor	Fold induction
1 x W2	770	8914	
2 x W2	998	46651	11
4 x W2	2375	105685	46
8 x W2	7680	164454	44
			21

W2 is the strongest elicitor-responsive *cis*-acting element that has been so far tested, eight copies of W2 giving GUS values of approximately 164,000.

4.3 Box N

Box N comes from the potato *gst1* gene (TTCTAGCCACCAGATTGACCAAAC; SEQ ID NO: 9) and has never previously been defined. It contains both an S Box sequence (AGCCACCAGA) and a W Box sequence (TTGACC) within just 25 base pairs and as such represents a novel *cis*-element composed of two types of elicitor response element within a very small stretch of DNA. A tetramer of Box N gives at least 75-fold elicitor inducibility. This observation suggests three important conclusions; firstly that Box N may be extremely useful for biotechnological applications, secondly that the core Box S sequence is AGCCACCANA (SEQ ID NO: 14) and thirdly that Boxes S and W may represent a common theme in plant promoters that respond to pathogens as these elements are present in both parsley and potato. Box N alone is a strong elicitor-responsive element and extremely interesting, as it consists of an S Box (GCCACC) followed by a W Box (TTGACC). The sequence of the element used (the monomer) is: 5'-actagtTTCTAGCCACCAGATTGACCAAACtctaga-3' with the element in upper case letters and the SpeI/XbaI ends in lower case letters. A construct with four copies of Box N was tested in transient expression assay. The results were as follows.

	minus elicitor	Plus elicitor	Fold induction
4 x N	1085	92980	85

Box N is a strong element and shows a very high fold inducibility. This novel combination and spacing of W and S Box elements may prove to be very useful for biotechnological purposes.

4.4 Box W_{Amy}

Box W_{Amy} comes from the wild oat α -Amy2/A and wheat α -Amy2/54 genes where it has previously been published under the name Box 2 or O2S (see Rushton, Plant Mol. Biol. 29 (1995), 691-702). It is a *cis*-acting element required for the transcriptional activation of these genes during germination but has never previously been linked to a role in pathogenesis. Box W_{Amy} consists of two W Box elements: a hexamer 5'-TTGACC-3' embedded in a palindromic 5'-TGAC-N₆-GTCA-3'. As it contains both types of sequences together it constitutes a new type of W Box and may be a "super W Box".

The sequence of the element used (the monomer) is: 5'-actagtGGATTGACTTGACCGTCATCGGCTtctaga-3' with the element in upper case letters and the SpeI/XbaI ends in lower case letters. A construct containing 7 copies of Box W_{Amy} was constructed and to the transient expression assay. The result is shown below.

	minus elicitor	Plus elicitor	Fold induction
7 x W _{Amy}	168	43867	260

W_{Amy} is a strong elicitor-responsive *cis*-acting element and has the highest fold induction of any W Box that has been so far tested. This element could therefore be a particularly effective W Box and could aid the designing of synthetic W Boxes that are even more effective.

Example 5: Synthetic promoters consisting of combinations of the above-described elements

Synthetic promoters composed of combinations of the above elicitor-responsive elements have never before been constructed or tested. All elements (Boxes W1, W2, S, U, D, N and W_{Amy}) are active in combination with each other; monomer, dimer and tetramer constructs being active. The furthest downstream element (nearest to the TATA Box) has the strongest effect on the synthetic promoter with further upstream elements having a much lesser effect. However the combination of two or more different types of *cis*-element may have a much more profound effect on expression *in planta*. In addition the insertion of a spacer region composed of anything between 100 base pairs and 1,000 base pairs appears to increase the contribution of the more upstream *cis*-elements. All of these synthetic promoters are good candidate promoters that may be rapidly and locally responsive to pathogen attack but also show negligible activity in uninfected tissues. These promoters may therefore allow the engineering of defence reactions that are closely related to natural defence mechanisms without appreciable activity in non-infected cells of the plant.

A large number of combinations have been tested. The results for some of these are detailed below. All of these combinations are novel and these constructs represent true synthetic promoters. The elements are inserted into the Spel/XbaI sites, as with all of the constructs, and read from the 5' end to the 3' end i.e 4 x W2/ 4 x S is:

Spel - W2- W2 - W2 - W2 - S- S -S -S- XbaI

Generally, the elements nearest to the TATA Box (i.e at the 3' end) have the greatest effect on both level of expression and fold induction. The effect of the upstream elements is often minimal and there is also an inhibitory effect probably due to steric hinderance when different elements are put close together; compare 4 x S/ 4 x W2 with (2 x S/ 2 x W2) x 2. The insertion of spacer regions between

elements is therefore recommended to alleviate problems due to steric hinderance. The results of the transient expression assays are shown below.

	minus elicitor	Plus elicitor	Fold induction
1 x S/ 1 x W2	1732	85126	49
2 x S/ 2 x W2	1529	95872	62
4 x S/ 4 x W2	2654	64105	24
(2 x S/ 2 x W2) x 2	483	9832	20
4 x W2/ 4 x S	2753	205826	74
1 x W2/ 1 x S	146	2690	18
2 x S/ 2 x D	191	15541	81
4 x S/ 4 x D	9775	100265	10
1 x D/ 1 x S	32	1246	38
4 x D/ 4 x S	6795	204115	30
2 x W2/ 2 x D	1762	32462	18
4 x W2/ 4 x D	22042	92875	4.2
4 x D/ 4 x W2	18857	276456	14
1 x D/ 1 x W2	295	4369	14

Adding more copies of an element in a composite construct often increases the absolute level of expression (e.g 2 x W2/ 2 x D and 4 x W2/ 4 x D) but often lowers the fold induction. In some cases even the absolute level of expression decreases (e.g 2 x S/ 2 x W2 and 4 x S/ 4 x W2) and a comparison with (2 x S/ 2 x W2) x 2 suggests that this is due to steric hinderance as the number of copies of the elements is the same, it is just the order that is changed.

Example 6: Transgenic plants carrying chimeric promoters

Transformants were tested for the response of the synthetic promoters to pathogens. Cultures of the bacterium *pseudomonas* (strains *Rpt2* or *Rpm1*) were grown in King's-B Medium containing 30 µg/ml kanamycin and 100µg/ml rifampicin. The bacteria were resuspended in 10mM MgCl₂ at an OD₆₀₀ of 0.2 and infiltrated into leaves via a syringe. Controls were performed using 10mM MgCl₂ alone. After 6 hours the leaves were removed from the plants and stained for GUS activity using X-Gluc. The expression pattern observed in the transgenic plants containing the GUS marker gene under the control of the chimeric promoter of the invention revealed expression in tissue infected by *Pseudomonas syringae* and in some cases also local expression in wounded tissues.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Max-Planck-Gesellschaft zur Förderung der
Wissenschaften e. V.

(B) STREET: none
(C) CITY: Berlin
(D) STATE: none
(E) COUNTRY: Germany
(F) POSTAL CODE (ZIP): none

(ii) TITLE OF INVENTION: Chimeric promoters capable of
mediating local gene expression in plants upon pathogen
infection

(iii) NUMBER OF SEQUENCES: 15

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

7

TTTGACC

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
CACACTTAAT TTGACCGAGT AACATTGCC

30

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
TTCAGCCNNN NNNNTTGACC

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
TTATTCAGCC ATCAAAGTTG ACCAATAAT

29

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

12-11-1998

42

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

14

TGACNNNNNN GTCA

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

14

TGACTTGACC GTCA

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

24

CAGCCACCAA AGAGGACCCA GAAT

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCCACCNNT TTGACC

16

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTCTAGCCAC CAGATTTGAC CAAAC

25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATTGACTT GACCGTCATC GGCT

24

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TACAATTCAA ACATTGTTCA AACAGGAAC C

31

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGTTGAAATT CAATA

15

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

AGTTGAAATT CAATAAGTTG AAATTCAATA

30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGCCACCANA

10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AGGTGGCACT TTTGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT TCTAAATACA	60
TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAT AATATTGAAA	120
AAGGAAGAGT ATGAGTATTAC AACATTTCCG TGCGCCCTT ATTCCCTTT TTGCGGCATT	180
TTGCCTTCCT GTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA	240
GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG	300
TTTCGCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC	360
GGTATTATCC CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA	420
GAATGACTTG GTTGAGTACT CACCAAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	480
AAGAGAATTAA TGCAGTGCTG CCATAACCAC GAGTGATAAC ACTGCGGCCA ACTTACTTCT	540

GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTG CACAACATGG GGGATCATGT 600
 AACTCGCCTT GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA 660
 CACCACGATG CCTGTAGCAA TGGCAACAAC GTTGCACAA CTATTAACGT GCGAACTACT 720
 TACTCTAGCT TCCCGAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 780
 ACTTCTGCAC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAACTG GAGCCGGTGA 840
 GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT GGTAAGCCCT CCCGTATCGT 900
 AGTTATCTAC ACGACGGGA GTCAGGCAAC TATGGATGAA CGAAATAGAC AGATCGCTGA 960
 GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT 1020
 TTAGATTGAT TTAAAACCTTC ATTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTGA 1080
 TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTCACTGAGCGT CAGACCCCCT 1140
 AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG CGCGTAATCT GCTGCTTGCA 1200
 AACAAAAAAA CCACCGCTAC CAGCGGTGGT TTGTTGCCG GATCAAGAGC TACCAACTCT 1260
 TTTTCCGAAG GTAACTGGCT TCAGCAGAGC GCAGATAACCA AATACTGTCC TTCTAGTGTA 1320
 GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT 1380
 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTTGGACTC 1440
 AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA ACAGGGGGTT CGTCACACAC 1500
 GCCCAGCTTG GAGCGAACGA CCTACACCGA ACTGAGATAC CTACAGCGTG AGCATTGAGA 1560
 AAGCGCCACG CTTCCCGAAG GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGCTGG 1620
 AACAGGAGAG CGCACCGAGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT 1680
 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGATGA TGCTCGTCAG GGGGGCGGAG 1740
 CCTATGGAAA AACGCCAGCA ACAGCGGCTT TTTACGGTTC CTGGCCTTT GCTGGCCTTT 1800
 TGCTCACATG TTCTTCCTG CGTTATCCCC TGATTCTGTG GATAACCGTA TTACCGCCTT 1860
 TGAGTGAGCT GATAACCGTC CCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA 1920
 GGAAGCGGAA GAGCGCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCACTTA 1980
 ATGCAGCGGA TCAAGCTTGG ATCCATCGAT GAATCGCG CGCCACTAGT GCCGGCCTGC 2040
 AGTCTAGAGT CGACCGCAAG ACCCTTCCTC TATATAAGGA AGTCATTTC ATTTGGAGAG 2100
 GACACGCTCG AGTGGCCACC ATGGTCCGTC CTGTAGAAAC CCCAACCGT GAAATCAAAA 2160
 AACTCGACGG CCTGTGGCA TTCAGTCTGG ATCGCGAAAA CTGTGGAATT GATCAGCGTT 2220

GGTGGGAAAG CGCGTTACAA GAAAGCCGGG CAATTGCTGT GCCAGGCAGT TTTAACGATC	2280
AGTTGCCGA TGCAGATATT CGTAATTATG CGGGCAACGT CTGGTATCAG CGCGAAGTCT	2340
TTATACCGAA AGGTGGCA GGCCAGCGTA TCGTGCTGCG TTTCGATGCG GTCACTCATT	2400
ACGGCAAAGT GTGGGTCAAT AATCAGGAAG TGATGGAGCA TCAGGGCGGC TATAGCCAT	2460
TTGAAGCCGA TGTCACGCCG TATGTTATTG CCGGGAAAAG TGTACGTATC ACCGTTGTG	2520
TGAACAACGA ACTGAACTGG CAGACTATCC CGCCGGGAAT GGTGATTACC GACGAAAACG	2580
GCAAGAAAAA GCAGTCTTAC TTCCATGATT TCTTTAACTA TGCCGGAATC CATCGCAGCG	2640
TAATGCTCTA CACCACGCCG AACACCTGGG TGGACGATAT CACCGTGGTG ACGCATGTCG	2700
CGCAAGACTG TAACCACCGCG TCTGTTGACT GGCAGGTGGT GGCCAATGGT GATGTCAGCG	2760
TTGAACTGCG TGATGCGGAT CAACAGGTGG TTGCAACTGG ACAAGGCACT AGCGGGACTT	2820
TGCAAGTGGT GAATCCGCAC CTCTGGCAAC CGGGTGAAGG TTATCTCTAT GAACTGTGCG	2880
TCACAGCCAA AAGCCAGACA GAGTGTGATA TCTACCCGCT TCGCGTCGGC ATCCGGTCAG	2940
TGGCAGTGAA GGGCGAACAG TTCTTGATTA ACCACAAACC GTTCTACTTT ACTGGCTTG	3000
GTCGTCATGA AGATGCGGAC TTGCGTGGCA AAGGATTCGA TAACGTGCTG ATGGTGCACG	3060
ACCACGCATT AATGGACTGG ATTGGGGCCA ACTCCTACCG TACCTCGCAT TACCCCTTACG	3120
CTGAAGAGAT GCTCGACTGG GCAGATGAAC ATGGCATCGT GGTGATTGAT GAAACTGCTG	3180
CTGTCGGCTT TAACCTCTCT TTAGGCATTG GTTTCGAAGC GGGCAACAAG CCGAAAGAAC	3240
TGTACAGCGA AGAGGCAGTC AACGGGGAAA CTCAGCAAGC GCACTTACAG GCGATTAAAG	3300
AGCTGATAGC GCGTGAACAA AACCAACCAA GCGTGGTGAT GTGGAGTATT GCCAACGAAC	3360
CGGATAACCG TCCGCAAGGT GCACGGGAAT ATTCGCGCC ACTGGCGGAA GCAACGCGTA	3420
AACTCGACCC GACCGCGTCCG ATCACCTGCG TCAATGTAAT GTTCTGCGAC GCTCACACCG	3480
ATACCATCAG CGATCTCTTT GATGTGCTGT GCCTGAACCG TTATTACGGA TGGTATGTCC	3540
AAAGCGGCGA TTTGGAAACG GCAGAGAAGG TACTGGAAAA AGAACTTCTG GCCTGGCAGG	3600
AGAAAATGCA TCAGCCGATT ATCATCACCG AATACGGCGT GGATACGTTA GCCGGGCTGC	3660
ACTCAATGTA CACCGACATG TGGAGTGAAG AGTATCAGTG TGCATGGCTG GATATGTATC	3720
ACCGCGTCTT TGATCGCGTC AGCGCCGTG TCGGTGAACA GGTATGGAAT TTCGCCGATT	3780
TTGCGACCTC GCAAGGCATA TTGCGCGTTG GCGGTAACAA GAAAGGGATC TTCACTCGCG	3840

ACCGCAAACC GAAGTCGGCG GCTTTCTGC TGCAAAACG CTGGACTGGC ATGAACCTCG	3900
GTGAAAACC GCAGCAGGGA GGCAAACAAT GAATCAACAA CTCTCCTGGC GCACCATCGT	3960
CGCTACAGCC TCGGGATTG CTACCGAGCT CCCGGTACC TGATCATGAG TAATTAGCTC	4020
GAATTCCCC GATCGTCAA ACATTTGGCA ATAAAGTTTC TTAAGATTGA ATCCTGTTGC	4080
CGGTCTTGCATGATTATCA TATAATTCT GTTGAATTAC GTTAAGCATG TAATAATTAA	4140
CATGTAATGC ATGACGTTAT TTATGAGATG GGTTTTATG ATTAGAGTCC CGCAATTATA	4200
CATTTAATAC GCGATAGAAA ACAAAATATA GCGCGCAAAC TAGGATAAAAT TATCGCGCGC	4260
GGTGTCATCT ATGTTACTAG ATCGGGATT AGATCTGCT	4299

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Max-Planck-Institut zur Förderung
der Wissenschaften e.V.
u. Z.: C 1078 EP

EPO - Munich
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12. Nov. 1998

CLAIMS

1. A chimeric promoter capable of mediating local gene expression in plants upon pathogen infection comprising
 - (i) at least one cis-acting element sufficient to direct elicitor-specific expression comprising the nucleotide sequence of any one of SEQ ID NOS: 3 to 14, and
 - (ii) a minimal promoter.
2. The chimeric promoter of claim 1, further comprising a cis-acting element having the nucleotide sequence of SEQ ID NO: 1 or 2.
3. The chimeric promoter of claim 1 or 2, wherein said synthetic plant promoter comprises homo- and/or hetero-multimeric forms of said cis-acting element(s).
4. The chimeric promoter of any one of claims 1 to 3, wherein said multimeric form is a dimer or tetramer.
5. The chimeric promoter of any one of claims 1 to 4, wherein the minimal promoter is derived from the CaMV35S promoter, CHS promoter, PR1 promoter, or hcbt2 promoter.
6. The chimeric promoter of any one of claims 1 to 5, wherein the distance between said cis-acting element and said minimal promoter is 25 to 70 base pairs.

7. The chimeric promoter of any one of claims 1 to 6, wherein a spacer region composed of 4 to 10 base pairs separates at least two of said cis-acting elements.
8. The chimeric promoter of any one of claims 3 to 7, wherein at least two of said multimeric forms are separated by a spacer of between about 50 to 1000 base pairs.
9. The chimeric promoter of any one of claims 1 to 8, wherein the induction of gene expression upon elicitor treatment or pathogen infection is at least 15-fold.
10. A recombinant gene comprising the chimeric promoter of any one of claims 1 to 9.
11. The recombinant gene of claim 10, wherein the chimeric promoter is operatively linked to a heterologous DNA sequence.
12. The recombinant gene of claim 10 or 11, wherein at least one of said cis-acting elements is located in the 5'- or 3'-untranslated region or in an intron of the recombinant gene.
13. The recombinant gene of any one of claims 10 to 12, wherein said heterologous DNA sequence encodes a (poly)peptide, cytotoxic protein, antibody, antisense RNA, sense RNA, ribozyme or transcription factor.
14. A vector comprising the chimeric promoter of any one of claims 1 to 9 or the recombinant gene of any one of claims 10 to 13.
15. A method for the production of transgenic plants, plant cells or plant tissue comprising the introduction of a chimeric promoter of any one of claims 1 to 9,

a recombinant gene of any one of claims 10 to 13 or the vector of claim 14 into the genome of said plant, plant cell or plant tissue.

16. Plant cells comprising a chimeric promoter of any one of claims 1 to 9, the recombinant gene of any one of claims 10 to 13 or the vector of claim 14 or obtainable by the method of claim 15.
17. A transgenic plant or plant tissue comprising plant cells of claim 16.
18. The transgenic plant of claim 17, which upon the presence of the chimeric promoter or the recombinant gene attained resistance or improved resistance against a pathogen the corresponding wild-type plant was susceptible to.
19. Harvestable parts of a transgenic plant of claim 17 or 18 comprising plant cells of claim 16.
20. Propagation material of a transgenic plant of claim 17 or 18 comprising plant cells of claim 16.
21. A cis-acting element as defined in claim 1 or a multimeric form(s) of any one of those as defined in claim 3 or 4.
22. A method for the identification of an activator or inhibitor of genes specifically expressed in plants upon pathogen infection comprising the steps of:
 - (a) providing a plant, plant cell, or plant tissue comprising a recombinant DNA molecule comprising a readout system operatively linked to the chimeric promoter of any one of claims 1 to 9;
 - (b) culturing said plant cell or tissue or maintaining said plant in the presence of a compound or a sample comprising a plurality of compounds under conditions which permit expression of said readout system;

- (c) identifying or verifying a sample and compound, respectively, which leads to suppression or activation and/or enhancement of expression of said readout system in said plant, plant cell, or plant tissue.

23. The method of claim 22 further comprising the step of

- (d) subdividing the samples identified in step (c) and repeating steps (a) to (c) one or more times.

24. The method of claim 22 or 23 further comprising the step of

- (e) identifying and/or isolating from the identified sample the compound responsible for said suppression or activation and/or enhancement of expression of said readout system in said plant, plant cell, or tissue.

25. The method of any one of claims 22 to 24, wherein

- (a) said recombinant DNA molecule is a recombinant gene of any one of claims 10 to 13 or a vector of claim 14;
- (b) said plant cell is a plant cell of claim 16;
- (c) said plant tissue is a plant tissue of claim 17, or
- (d) said plant is a plant of claim 17 or 18.

26. A method for preparing a plant elicitor comprising the steps of the method of any one of claims 22 to 25 and formulating the compound obtained or identified in step (c) or (e) in a form suitable for the application in agriculture or plant cell and tissue culture.

27. A compound obtained or identified by the method of any one of claims 22 to 26 which is an activator or inhibitor of gene expression and/or function in plants.

28. An antibody specifically recognizing the compound of claim 27 or the cis-acting element of claim 21.

29. A diagnostic composition comprising a chimeric promoter of any one of claims 1 to 9, the recombinant gene of any one of claims 10 to 13, the vector of claim 14, the compound of claim 27 or the antibody of claim 28, and optionally suitable means for detection.
30. A kit comprising a chimeric promoter of any one of claims 1 to 9, the recombinant gene of any one of claims 10 to 13, the vector of claim 14, the compound of claim 27 or the antibody of claim 28.
31. A plant protection composition comprising the compound of claim 27.
32. Use of a cis-acting element sufficient to direct elicitor-specific expression, a chimeric promoter of any one of claims 1 to 9, the recombinant gene of any one of claims 10 to 13, the vector of claim 14, the cis-acting element of claim 21 and/or the compound of claim 27 for the production of pathogen resistant plants.
33. Use of a cis-acting element sufficient to direct elicitor-specific expression, the chimeric promoter of any one of claims 1 to 9, a recombinant gene of any one of claims 10 to 13, a vector of claim 14, the plant cell of claim 16, the plant tissue of claim 17, or the plant of claim 17 or 18 for identifying and/or producing compounds capable of conferring induced resistance to a pathogen in a plant.
34. A method of rendering a gene responsive to pathogens comprising inserting at least one cis-acting element sufficient to direct elicitor-specific expression into the promoter of said gene.
35. A method for preparing a promoter capable of mediating local gene expression in plants upon pathogen infection comprising operably linking a

cis-acting element sufficient to direct elicitor-specific expression to a transcription initiation sequence of a promoter.

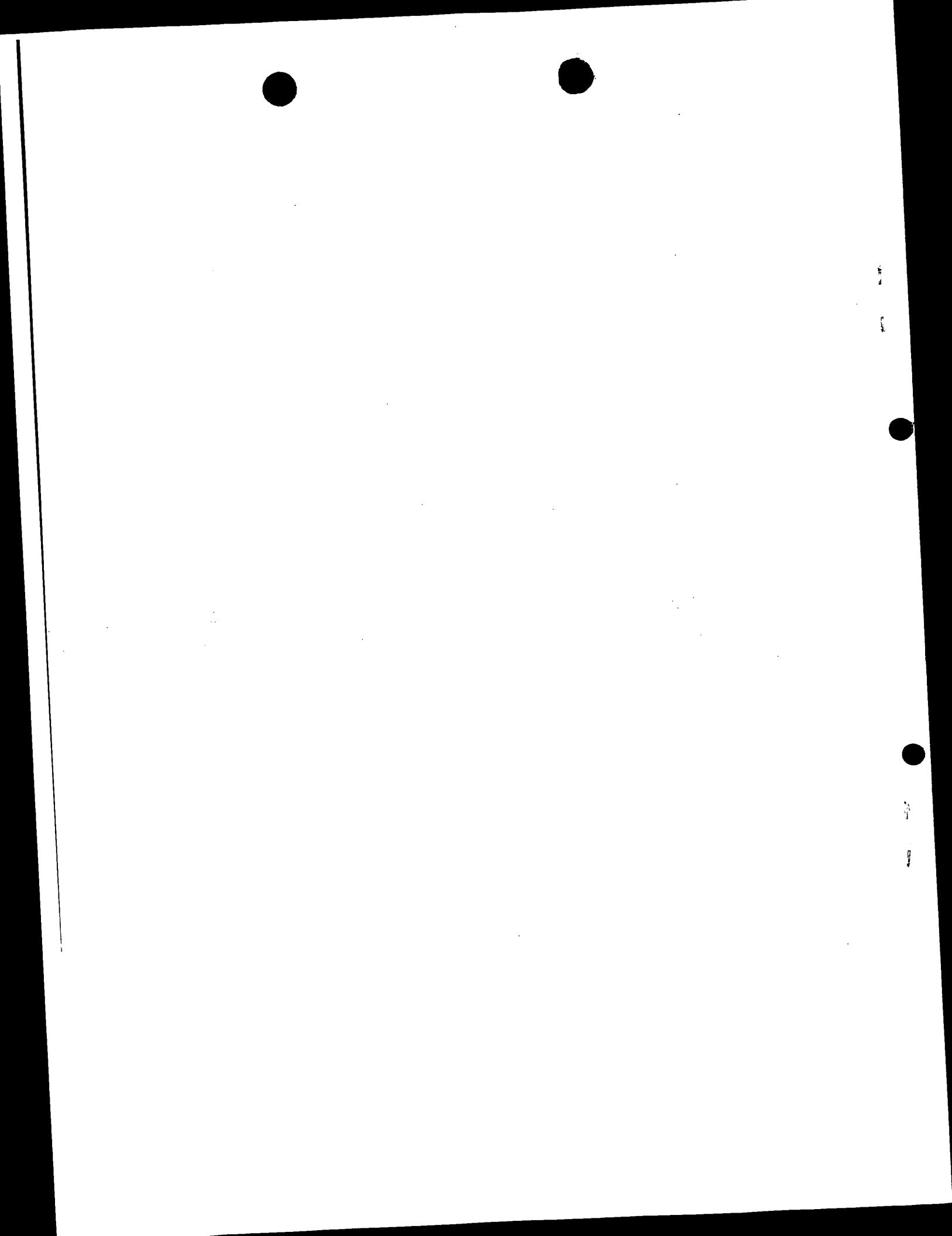
36. The method of claim 34 or 35, wherein said cis-acting element is a cis-acting element as defined in claim 1 or 2 or a multimeric form thereof as defined in any one of claims 3 to 8.
37. The method of any one of claims 34 to 36, further comprising deleting non-specific cis-acting elements in the promoter.
38. The promoter obtainable by the method of any one of claims 34 to 37.
39. Use of the compound of claim 27 as plant protective agent or herbicide.

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Abstract

Described are synthetic promoter capable of mediating gene expression in plants upon pathogen infection. Furthermore, recombinant genes and vectors comprising said chimeric promoters as well as host cells transformed with such chimeric promoters, recombinant genes or vectors are provided. Additionally, diagnostic compositions and kits comprising such chimeric promoters, recombinant genes, vectors or cells are described. Provided are further methods for the identification of compounds being capable of activating or inhibiting genes that are specifically expressed in plants upon pathogen infection employing the above described means. Furthermore, transgenic plant cells, plant tissue and plants containing the above-described chimeric promoters, recombinant genes and vectors as well as the use of the aforementioned chimeric promoters, recombinant genes, vectors and/or compounds identified by the method of the invention in plant cell and tissue culture, plant breeding and/or agriculture are described.



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Fig. 1

Restriction map of plasmid ms23

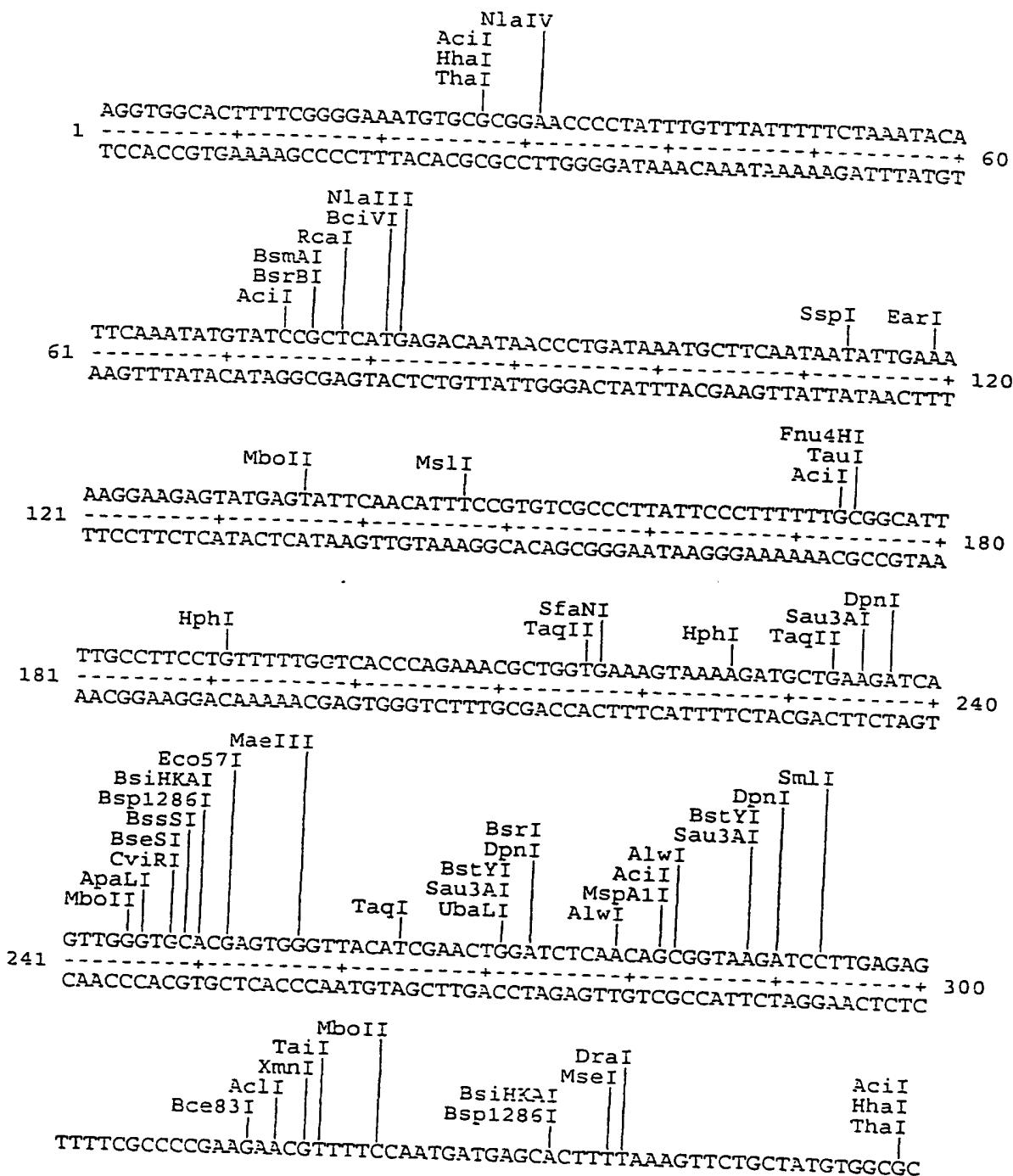


Fig. 1 (cont.)

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Fig. 1 (cont.) 301 360

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301 AAAAGCGGGGCTTCTGCAGAAAGGTTACTACTCGTGAATTCAGACGATAACCGCG
      +-----+
      HgaI
      TaqII
      NciI
      ScrFI
      MspI
      BcgI
      BscGI BsaHI
      +-----+
      GGTATTATCCGTATTGACGCCGGCAAGAGCAACTCGTCGCCGATACACTATTCTA
      +-----+
      361 CCATAATAGGGCATAACTGCGCCGTTCTCGTTAGCCAGCGCGTATGTGATAAGAGT
      +-----+
      RsaI
      ScaI
      MaeIII
      TatI
      HphI
      Tsp45I
      BsrI
      +-----+
      GAATGACTTGGTTGAGTACTCACCAAGTCACAGAAAAGCATCTTACGGATGGCATGACAGT
      +-----+
      421 CTTACTGAACCAACTCATGAGTGGTCAGTGTCTTCGTTAGAATGCCTACCGTACTGTCA
      +-----+
      FokI
      BccI
      Bst4CI
      SfaNI
      NlaIII
      +-----+
      CviJI
      HaeIII
      TspRI
      EaeI
      Fnu4HI
      GdiII
      TauI
      AcI
      BtsI
      CjePI
      +-----+
      Tsp509I
      BbvI
      CviRI
      BtsI
      TspRI
      Fnu4HI
      TseI
      +-----+
      AAGAGAATTATGCAGTGCTGCCATAACCAGTACAGTACAGAAAAGCATCTTACGGATGGCATGACAGT
      +-----+
      481 TTCTCTTAATACGTACGACGGTATTGGTACTCACTATTGTGACGCCGGTTGAATGAAGA
      +-----+
      AlwI
      NlaIII
      MaeIII
      DpnI
      Sau3AI
      CviRI
      NlaIII
      +-----+
      AvaII
      Sau96I
      CjePI
      BsiI
      PvuI
      DpnI
      Sau3AI
      Mn1I
      +-----+
      GACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTGACAAACATGGGGATCATGT
      +-----+
      541 CTGTTGCTAGCCTCCTGGCTTCCTCGATTGGCAAAAAACGTGTTGACCCCCCTAGTACA
      +-----+
      AlwI
      NlaIII
      MaeIII
      DpnI
      Sau3AI
      CviRI
      NlaIII
      +-----+
      AceIII
      DpnI
      Sau3AI
      MspI
      BsaWI
      NlaIV
      AluI
      CviJI
      CviJI
      +-----+
      AACTCGCTTGATCGTTGGAACCGGAGCTGAATGAAGCCATACCAACGACCGAGCGTGA
      +-----+
      601 TTGAGCGGAACTAGCAACCCTGGCCTCGACTTACTTCGGTATGGTTGCTGCTCGCACT
      +-----+
      SfaNI
      MaeIII
      Tsp45I
      +-----+
      HhaI
      FspI
      TaiI
      BsrDI
      AcI
      +-----+
      MsI
      SfcI
      +-----+
      CACCAACGATGCCTGTAGCAATGGCAACAAACGTTGCGCAACTATTAACGGCGAACTACT
      +-----+
      661 GTGGTGCTACGGACATCGTTACCGTTGCAACCGCGTTGATAATTGACCGCTTGATGA
      +-----+
      MseI
      BsrI
      +-----+
      MseI
      +-----+
      72
  
```

Fig. 1 (cont.)

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721 Tsp509I VspI
 AluI MspI CviJI NciI BfaI ScrFI MnII BccI BsRI EcII AcII Foki AvaiI Sau96I CvIRI
 TACTCTAGCTTCCCGCAACAAATTAAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACC
 ATGAGATCGAAGGCCGTTGTTAATTATCTGACCTACCTCCGCCTATTCAACGTCCTGG

 781 CviJI Cac8I CviJI HaeIII BgI MspI MwoI MsPI BsrFI CvIRI NlaIV
 HhaI Sau96I HaeIII BgI MspI MwoI MsPI BsrFI CvIRI NlaIV
 ACTTCTGCGCTCGGCCCTCCGGCTGGCTGGTTATTGCTGATAAAATCTGGAGCCGGTGA
 TGAAGACGCGAGCCGGAGGCCGACCGACCAAATAACGACTATTTAGACCTCGGCCACT 840

 41 AciI BsaI BsmAI ThaI BpmI Hphi SimI BsrDI TseI Fnu4HI CviRI Sau96I BccI BfI BbvI CviJI HaeIII BsrI NlaIV TspRI CviJI BscGI MnII Pf11108I
 Hin4I GCGTGGGTCTCGCGGTATCATTGCAGCACTGGGCCAGATGGTAAGCCCTCCCCTGATCGT 900
 CGCACCCAGAGGCCATAGTAACGTCGTGACCCGGTCTACCATTGGAGGGCATAGCA

 1 HinfI Ahdi HaeIV Hin4I BscGI PleI BseMII DpnI
 AGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGA
 TCAATAGATGTGCTGCCCTCAGTCCGTTGATAACCTACTGCTTATCTGTCTAGCGACT 960

 1 NlaIV MnII MspI TspRI MaeIII Bst4CI CjePI DpnI
 BanI GATAGGTGCCTCACTGATTAAGCATTGGTAAGTCAGACCAAGTTACTCATATATACT
 CTATCCACGGAGTGACTAATCGTAACCATTGACAGTCTGGTTCAAATGAGTATATGA 1020

 CjePI DraI MspI Tsp509I DraI MspI DpnI BstYI Sau3AI
 TTAGATTGATTTAAACTTCATTAAATTAAAGGATCTAGGTGAAGATCCTTTTGA
 AATCTAACTAAATTGAAAGTAAAAATTAAATTTCCTAGATCCACTCTAGGAAAAC 1080

Fig.1 (cont.)

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1081 TAATCTCATGACCAAAATCCCTAACGTGAGTTTCGTTCCACTGAGCGTCAGACCCCGT
 RcaI NlaII MseI TaiI Bsp24I CjePI CjeI UbaLI TspRI BseMII DdeI SimI BscGI 1140
 ATTAGAGTACTGGTTTAGGAATTGCACTAAAAAGCAAGGTGACTCGCAGTCTGGGGCA

1141 AGAAAAAGATCAAAGGATCTTCTTGAGATCCTTTCTGCGCGTAATCTGCTGCTTGCA
 Sau3AI Bsp24I BstYI DpnI Sau3AI BstYI DpnI Tth111II Bce83I Hhai Thai Fnu4HI TseI CviRI Cac8I 1200
 CjeI CjePI Bsp24I Sau3AI BstYI DpnI Tth111II Bce83I Hhai Thai Fnu4HI TseI MwoI CviRI Cac8I
 TCTTTCTAGTTCCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGT

1201 AACAAAAAAACCACCGCTACCAGCGGTGGTTTGCCGGATCAAGAGCTACCAACTCT
 CjeI Tth111II HgIeII AcII MspAII AluI CviJI AlwI 1260
 TTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATAACAAATACTGTCCTTAGTGTA
 Eco57I MaeIII BsrI CviJI Bsp24I CjePI CjeI BcefI Bst4CI BfaI CjePI 1320
 AAAAGGCTTCATTGACCGAAGTCGTCTCGCTATGGTTATGACAGGAAGATCACAT

1321 CjeI CjePI HaeI CviJI HaeIII SfcI AciI MnI
 Bsp24I CviJI BsII BsrI CjePI CjeI BcefI Bst4CI BfaI CjePI 1380
 GCCGTAGTTAGGCCACCACTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCT
 CGGCATCAATCCGGTGGTGAAGTTCTGAGACATCGTGGGGATGTATGGAGCGAGACGA

1381 BsrI Fnu4HI TseI Fnu4HI TspRI AlwNI CviJI MmeI Bce83I MspI NciI PleI
 BbvI MaeIII BsrI TseI CviJI TspRI Bce83I ScrFI HinFI SmlI
 BbvI BsrI TseI CviJI TspRI MmeI Bce83I MspI NciI PleI
 AATCCTGTTACCACTGGCTGCCAGTGGCGATAAGTCGTCTTACCGGGTTGGACTC 1440
 TTAGGACAATGGTCACCGACGACGGTCACCGCTATTAGCACAGAATGGCCAACCTGAG

Fig.1 (cont.)

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1441 AAGACGATAGTTACCGGATAAGGCGCAGCGTCCGGCTGAACGGGGGTTCGTGCACACA
 TTCTGCTATCAATGGCCTATTCCGCGTCCAGCCCCACTTGCCCCCAAGCACGTGTGT 1500

1501 GCCCAGCTGGAGCGAACGACCTACACCGAACTGAGATACTACAGCGTGAGCATTGAGA
 CGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGTAACTCT 1560

1561 AAGGCCACGCTTCCCAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGG
 TTGCGGGTGCAGAGGGCTTCCCTTTCCGCCTGCCATAGGCCATTGCCGTCCCAGCC 1620

1621 AACAGGAGAGCGCACGAGGGAGCTTCCAGGGAAACGCCCTGGTATCTTATAGTCCGT
 TTGTCCTCTCGCGTGCCTCCCTCGAAGGTCCCCCTTGCGGACCATAGAAATATCAGGACA 1680

1681 CGGGTTCGCCACCTCTGACTTGGCTGGATTTGTGATGCTCGTCAGGGGGCGGAG
 GCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCTC 1740

1741 CCTATGGAAAACGCCAGCAACCGGGCTTTTACGGTTCTGGCCTTTGCTGGCCTT
 GGATACCTTTGCGGTCGGATGCCAAGGACCGGAAACGACCGGAAA 1800

1801 TGCTCACATGTTCTTCTGCCTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTT 1850

Fig. 1 (cont.) 6/15
 ACCAGGTGTACARGAATGGACGCCATAGGGGACTAACCTATTGGCATAATGGCGGAA

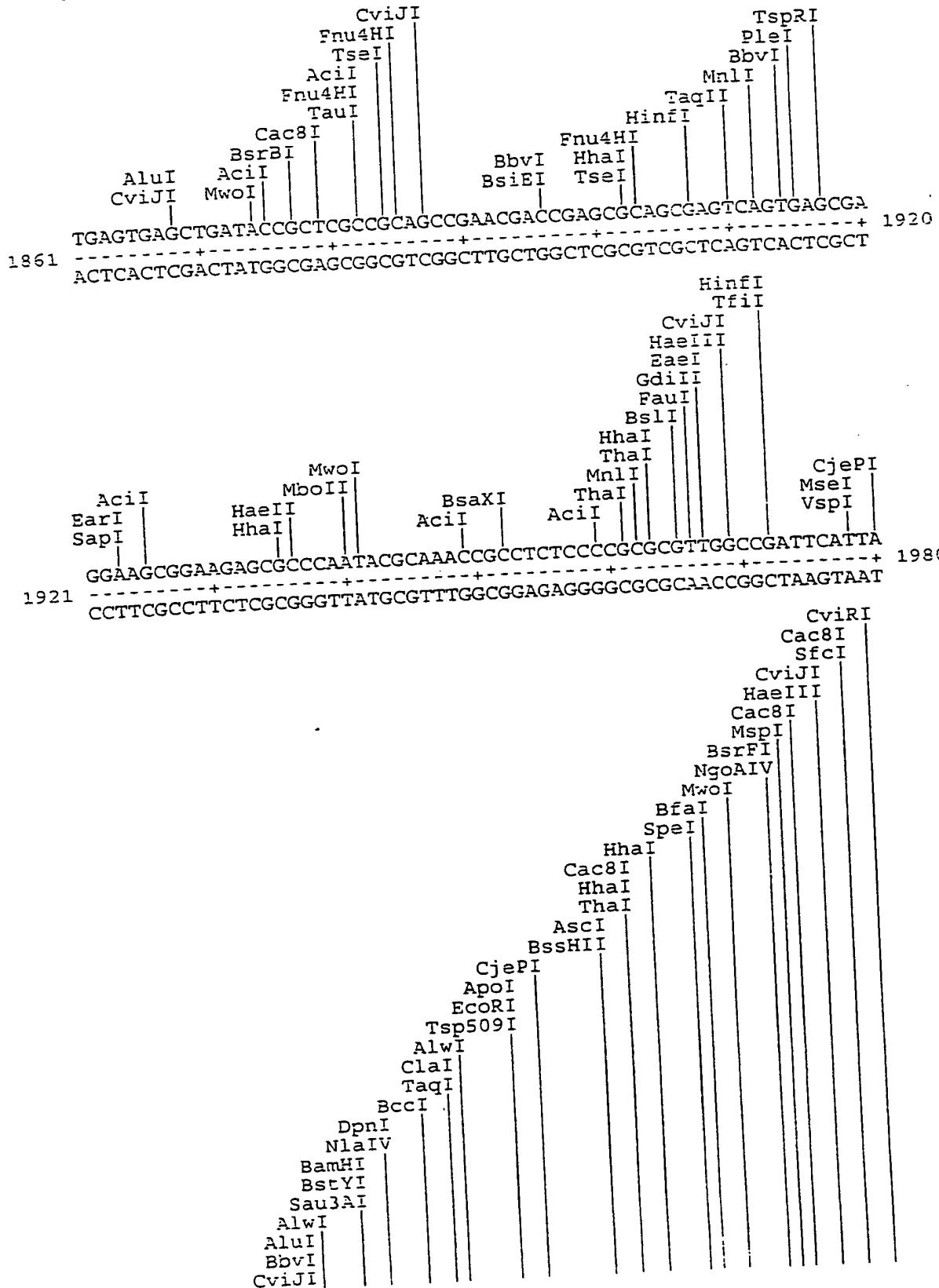


Fig. 1 (cont.)

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1981 ATGcagcGGATCAAGCTTGGATCCATCGATGAATTGGCGGCCACTAGTGCCGGCCTGC
 TACgtcgCCTAGTTGAAACCTAGGTAGCTACTTAAGCCGCGCGGTGATCACGGCCGGACG 2040
 2041 AGTCTAGAGTCGACCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTTCAATTGGAGAG
 TCAGATCTCAGCTGGCGTTCTGGGAAGGAGATATATTCCCTCAAGTAAAGTAAACCTCTC 2100
 2051 GACACGCTCGAGTGGCCACCATGGTCCGTCTGTAGAAACCCAACCCGTGAAATCAAAA
 CTGTGCGAGCTCACCGGTGGTACCAGGACATCTTGGGTTGGGCACTTTAGTTT 2160
 2061 AACTCGACGGCTGTGGGATTCAAGTCTGGATCGCGAAAATGTGGAATTGATCAGGCTT

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Fig. 1 (cont.)

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Fig.1 (cont.) 8/15 2220
 2161 TTGAGCTGCCGGACACCCGTAAGTCAGACCTAGCGCTTTGACACCTTAACTAGTCGCAA
 CjePI MunI SfaNI
 MaeIII Tsp509I DpnI
 HhaI NciI Sau3AI
 ThaI ScrFI MsI
 CviJI MspI EcorII
 FauI Cac8I HhaI
 CviRI Tsp509I AciI ThaI
 HaeI TaiI
 HaeIII Cac8I BbvI Fnu4HI
 HaeIII CviJI Sfani Tsp45I
 HaeIII HaeIII TseI MaeIII
 Cac8I MwoI TaqI AciI RleAI
 TTATACCGAAAGGTTGGGCAGGCCAGCGTATCGCTGCGTTCGATGCGGTCACTCATT 2340
 2281 AATATGGCTTCCAACCCGTCCGGTCGCATAGCACGACGCAAAGCTACGCCAGTGAGTAA
 BceFI CviJI Fnu4HI
 SimI HaeIV Sfani
 BceFI Hin4I TauI
 BccI AciI
 ACGGCAAAGTGTGGGTCAATAATCAGGAAGTGTGGAGCATCAGGCCGGCTACGCCAT 2400
 2341 TGCCGTTCACACCCAGTTATTAGTCCTCACTACCTCGTAGTCCGCCGATATGCGGTA
 BceFI CviJI Fnu4HI
 MaeIII Tsp45I HaeIV
 CviJI BccI Hin4I
 BceFI NciI Sfani
 BceFI ScrFI TauI
 BceFI MspI AciI
 TTGAAGCCGATGTCACGCCGTATGTTATTGCCGGAAAAGTGTACGTATCACCGTTGTG 2460
 2401 AACTTCGGCTACAGTGCAGCATACAATAACGCCCTTTCACATGCATAGGGCAAACAC
 BceFI NciI BsaAI
 CviJI ScrFI SnaBI
 BceFI MspI RsaI
 BceFI HphI Bst4CI
 CjePI TaiI
 BceFI FauI
 CjePI NciI
 CjePI ScrFI
 CjePI MspI
 BsrI AcI HphI
 BceFI BsrI
 NlaIII AcI
 MspI HphI
 GCAAGAAAAAGCAGTCTTACTTCATGATTCTTAACTATGCCGGAAATGGTATTACCGACGAAAACG 2520
 2461 TGAAACACGAACACTGAACTGGCAGACTATCCCGCCGGAAATGGTATTACCGACGAAAACG
 2521 ACTTGTGCTTGACTTGACCGTCTGATAGGGCGGCCCTTACCAACTAATGGCTGTTTGCG
 BceFI NlaIII MspI Hinfi Fnu4HI
 BceFI MspI Tfii TseI
 BceFI BccI
 GCAAGAAAAAGCAGTCTTACTTCATGATTCTTAACTATGCCGGAAATCCATCGCAGCG 2580
 2581 CGTTCTTTTCGTCAGAATGAGGTACTAAAGAAATTGATAACGCCCTTACGTAGCGTCGC

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Fig. 1 (cont.)

2641 TAATGCTCTACACCACGCCAACACCTGGGTGGACGATATCACCGTGGTGACGCATGTCG
 ATTACGAGATGTGGTGCCTGTTGGACCCACCTGCTATAGTGGCACCACGTGCGTACAGC 2700

BbvI TaqII EcoRII HphI EcoRV Bst4CI BsaJI BstDSI NlaIII PshAI ThaI HgaI HphI MwoI NspI

Bst4CI MaeIII AfI III HincII AarI CviJI HaeI HaeIII HaeI III MscI EaeI HphI

HhaI HgaI MluI BspMI BsrI BsrI FauI BfaI AcI I

CGCAAGACTGTAACCACCGCTCTGTTGACTGGCAGGTGGTGGCCAATGGTGATGTCAGCG 2760
 GCGTTCTGACATTGGTGCGCAGACA ACTGACCGTCCACCAACCGTTACCACTACAGTCG

SfaNI Sau3AI DpnI BsaBI AcI I AlwI CviRI BspGI BsrI FauI BfaI AcI I

TTGAACTGCGTGATGCGGATCAACAGGTGGTGGCAACTGGACAAGGCACTAGGGGGACTT 2820
 AACTTGACGCACTACGCCTAGTTGTCACCAACGTTGACCTGTTCCGTGATGCCCTGAA

CviRI BsmFI Hinfi TfI MspI NciI ScrFI Hgai HphI MaeIII Tsp45I Bst4CI

BsmFI AcI I HphI MwoI MnI BslI Hgai HphI Bst4CI

TGCAAGTGGTGAATCCGCACCTCTGGCAACCGGGTGAAGGTTATCTCTATGAACGTGCG 2880
 ACGTTCAACCACTAGGCGTGGAGACCGTTGGCCACTTCCAATAGAGATACTTGACACGC

CviJI CjeI CjeI CviJI AlwNI CjeI Hgai FokI FauI MspI BsI I BsaWI SfaNI

TCACAGCCAAAAGCCAGACAGAGTGTGATATCTACCCGCTTCGCGTCGGCATCCGGTCAG 2940
 AGTGTGGTTTCGGTCTGTCACACTATAGATGGCGAAGCGCAGCCGTAGGCCAGTC

BtsI TspRI TspRI Bst4CI CjeI MseI CjeI Bst4CI CjeI Bst4CI CjeI

TGGCAGTGAAGGGCGAACAGTTCCTGATTAACCACAAACCGTTCTACTTTACTGGCTTG 3000
 ACCGTCACCTCCCGCTTGTCAAGGACTAATTGGTGTGGCAAGATGAAATGACCGAAC

SfaNI RcaI NlaIII BcgI MboII TaqI HinfI TfiI ApaLI BsiHKAI Bsp1286I BsaSI CviRI

GTCGTCAAGATGCGGACTTGCCTGGCAAAGGATTGATAACGTGCTGATGGTGCACG 3060
 CAGCAGTACTTCTACGCCCTGAGCGACCGTTCCATAAGCTATTGCGACTACCAACGTG

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Fig.1 (cont.)

Sequence diagram showing restriction enzyme cleavage sites across several DNA fragments. The fragments are labeled by their start position (e.g., 3061, 3120, 3180, 3240, 3300, 3360, 3420, 3480) and end position (e.g., 3120, 3180, 3240, 3300, 3360, 3420, 3480). The sequence is represented by a dashed line with vertical tick marks indicating cleavage sites for various enzymes. The enzymes listed include: CviJI, HaeIII, NlaIV, Sau96I, Bsrl, RsaI, Bst4CI, MnII, SfaNI, EarI, VspI, MseI, BfiI, BbvI, Fnu4HI, TseI, HphI, MboII, Eco57I, NlaIII, MsI, SfaNI, TaqI, Bsrl, BbvI, TseI, HphI, CviJI, BcgI, MnII, NspV, Cac8I, CviJI, BcgI, CviJI, BcgI, MnII, FauI, TagI, AcI, Cac8I, CviJI, BcgI, MseI, RsaI, BsrGI, Bst4CI, TatI, BscGI, HincII, BseMII, HhaI, AceIII, MseI, MaeIII, Tsp45I, HhaI, BciVI, MspI, BsaWI, AluI, MwoI, CjeI, BsII, TaqII, HphI, CjeI, BscGI, BsrI, EcII, TspRI, ThaI, AfI, MluI, BscGI, BsiHKAI, Bsp1286I, BseSI, CviRI, ApaLI, SspI, HhaI, MwoI, AciI, BsrI, EcII, TspRI, ThaI, AfI, MluI, DpnI, HgaI, Sau3AI, HgaI, HphI, ThaI, SimI, TagI, AflII, MluI, AarI, BspMI, HgaI, CjePI.

3061 ACCACGCATTAAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACG 3120
 MseI VspI Sau96I Bsrl RsaI Bst4CI MnII SfaNI EarI
 ACCACGCATTAAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACG 3120
 3061 TGGTCGCTAATTACCTGACCTAACCCCCGGTTGAGGATGGCATGGAGCGTAATGGGAATGC
 MboII Eco57I NlaIII MsI BbvI TseI HphI
 CTGAAGAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTATTGATGAAACTGCTG 3180
 3121 GACTTCTCTACGAGCTGACCCGTCTACTTGTACCGTAGCACCAACTACTTGACGAC
 CviJI MseI BcgI MnII NspV Cac8I CviJI
 CTGTCGGCTTAACCTCTCTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAC 3240
 3181 GACAGCCGAAATTGGAGAGAAATCCGTAACCAAAGCTCGCCCGTTGGCTTGGCTTCTTG
 MnII EarI RsaI BsrGI Bst4CI TatI BscGI HincII BseMII HhaI AceIII MseI
 TGTACAGCGAAGAGGCAGTCAACGGGAAACTCAGCAAGCGCACTTACAGGGATTAAAG 3300
 3241 ACATGTCGCTTCTCCGTCA GTGCCCTTGAGTCGTTCGCGTGAATGTCCGCTAATTTC
 MaeIII Tsp45I HhaI BciVI MspI BsaWI
 AluI MwoI CjeI BsII TaqII HphI CjeI
 AGCTGATAGCGCGTGACAAAAACCACCCAAGCGTGGTGTGGAGTATTGCCAACGAAC 3360
 3301 TCGACTATCGCCACTGTTGGTGGTTCGCACCACTACACCTCATAACGGTTGCTTG
 BscGI BsrI EcII TspRI ThaI AfI MluI
 CGGATACCGTCCGCAAGGTGCACGGGAATATTCGCGCCACTGGCGGAAGCAACCGCTA 3420
 3361 GCCTATGGCAGGCCTTACGTGCCCTATAAGCGCGGTGACCGCCTTGTGCGCAT
 DpnI HgaI Sau3AI HgaI BsrI EcII TspRI ThaI AfI MluI
 SimI TagI AflII MluI AarI BspMI HgaI CjePI
 AACTCGACCCGACCGTCCGATCACCTCGCGTCAATGTAATGTTCTGCGACGCTCACACCG 3480
 3421 HphI ThaI HgaI AarI BspMI HgaI CjePI

Fig. 1 (cont.)

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TTGAGCTGGCCTGCGCAGGCTAGTGGACGCCAGTTACATTACAAGACCGCTGCGAGTGTGGC

3481 ATACCATCAGCGATCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCC
 TATGGTAGTCGCTAGAGAAACTACACGACACGGACTTGGCAATAATGCCCTACCATACAGG 3540

Fnu4HI
 TaaI
 AcII
 FokI
 AAAGCGGCGATTGGAAACGGCAGAGAAGGTACTGGAAAAAGAACCTCTGGCCTGGCAGG
 RsaI BceI BsrI
 TTTGCCGCTAACCTTGCCTCTTCATGACCTTTCTTGAAGACCGGACCGTCC 3600

3601 AGAAA~~CTG~~CATCAGCCGATTATCATCACCGAATA~~CGG~~GTGGATACGTTAGCCGGGCTGC
 TCTTTGACGTAGTCGGCTAAC~~AGT~~AGTAGTG~~GG~~CTTATGCCGCACCTATGCAATCGGCCCCGACG 3660

3721 ACCCGCGTCTTGATCGCGTCAGCGCCGTCGTCGGTGAACAGGTATGGAATTTCGCCGATT
 TGGCGCAGAAACTAGCGCAGTCGCGGCAGCAGCCACTTGTCCATACCTTAAAGCGGGCTAA 3780

3781 TTGCGACCTCGCAAGGCATATTGCGCGTTGGCGGTAAACAAGAAAGGGATCTTCACTCGCG
 AACGCTGGAGCGTTCGGTAAACGCGCAACGCCATTGTTCTTCCTAGAAGTGAGCGC 3840
 CviJI

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Fig. 1 (cont.)

Fnu4HI
 TauI
 AcII
 BsiEI
 BbvI
 CviRI
 Fnu4HI
 TseI
 BcgI
 BspGI
 MwoI
 NlaIII
 BsRI
 ACCGCAAAACCGAAGTCGGCGGCTTTCTGCTGCACCGTGGACTGGCATGAACCTTCG 3900
 3841 TGGCGTTGGCTTCAGCCGCCAAAAGACGACGTTTGCGACCTGACCGTACTTGAAGC

BsII
 BcgI
 Fnu4HI
 HphI
 MnII
 TseI
 AcII
 BbvI
 HinFI
 TfII
 Tth111II
 BcgI
 ScrFI
 EcoRII
 HhaI
 BccI
 GTGAAAAAACCGCAGCAGGGAGGCACAAATGAATCAACAPCTCTCCTGGCGCACCATCGT 3960
 3901 CACTTTGGCGTCGTCCCTCCGTTACTTAGTTGAGAGGACCGCGTGGTAGCA

Tsp509I
 NlaIII
 RcaI
 DpnI
 BclI
 Sau3AI
 KpnI
 NlaIV
 Rsal
 BanI
 NciI
 ScrFI
 SmaI
 MspI
 NciI
 ScrFI
 AvAI
 BsaJI
 BanII
 BsiHKAI
 Bsp1286I
 SacI
 AluI
 CviJI
 TaqI
 AluI
 CviJI
 CGCTACAGCCTCGGAATTGCTACCGAGCTcccggtacctgatcatgagtaatttagctC 4020
 3961 GCGATGTCGGAGCCCTTAACGATGGCTCGAGggccatggactgtactcattaatcgAG

Tsp509I
 AvaI
 BsaJI
 CviJI
 BcgI
 MnII
 BsiEI
 PvuI
 DpnI
 ApoI
 Tsp509I
 Sau3AI
 GAATTCCCCGATCGTTCAAACATTGGCAATAAGTTCTTAAGATTGAATCCTGTTGC 4080
 4021 CTTAAGGGGCTAGCAAGTTGTAACCGTTATTCAAGAATTCTAACTTAGGACAACG

MspI
 BsII
 BsrFI
 AfIII
 HinfI
 TfiI
 MspI
 BspLUIII
 MspI
 Tsp509I
 NlaIII
 NspI
 Tsp509I
 MspI
 TailI
 MspI
 MwoI
 BsaBI
 Tsp509I
 Tsp509I
 CGGTCTTGGATGATTATCATATAATTCTGTTGAATTACGTTAACGATGTAATAATTAA 4140
 4081 GCCAGAACGCTACTAATAGTATATTAAAGACAACTTAATGCAATTGTCACATTATTAA

Fig.1 (cont.)

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NlaIII
NsI
CviRI
NlaIII
NspI
TaaI
BsmFI
BccI
HinfI
Tsp509I
PleI
AciI
FauI
CATGTAATGCATGACGTTATTATGAGATGGGTTTTATGATTAGAGTCGGCAATTATA
4141 GTACATTACGTACTGCAATTAATACTCTACCCAAAATACTAATCTCAGGGCGTTAATAT 4200

MseI
ThaI
BssHII
HhaI
Cac8I
HhaI
ThaI
BfaI
HaeIV
Hin4I
Tsp509I
BssHII
Cac8I
HhaI
ThaI
CATTTAACGCGATAGAAAAACAAAATATAGCGCGCAAACTAGGATAATTATCGCGCGC
4201 GTAAATTATGCGCTATCTTTGTTTATATCGCGCTTGATCCTATTAATAGCGCGCG 4250

DpnI
BglII
BstYI
Sau3AI
Tsp509I
DpnI
Sau3AI
MaeIII
BfaI
GGTGTCACTATGTTACTAGATCGGGattagatctgctagc
4261 CCACAGTAGATAACAATGATCTAGCCCTtaatctagacgatcg 4302

Enzymes that do cut:

AarI	AccI	AceIII	AcI	AcII	AfIII	AfIIII	AhdI
AluI	AlwI	AlwNI	ApaLI	ApoI	AsCI	Avai	Avai
BamHI	BanI	BanII	BbVI	BccI	Bce83I	BcefI	BcgI
BciVI	BclI	BfaI	BfiI	BglI	BglII	BpmI	BsaI
BsaAI	BsABI	BsaHI	BsaJI	BsaWI	BsaXI	BscGI	BseMII
BseSI	BsgI	BsiEI	BsiHKAI	BslI	BsmI	BsmAI	BsmFI
Bsp24I	Bsp1286I	BspGI	BspLU11I	BspMI	BsrI	BsrBI	BsrDI
BsrFI	BsrGI	BssHII	BssSI	Bst4CI	BstDSI	BstYI	BtsI
Cac8I	CjeI	CjePI	ClaI	CviJI	CviRI	DdeI	DpnI
DraI	DrdI	EaeI	EarI	EcII	Eco57I	EcoRI	EcoRII
EcoRV	FauI	Fnu4HI	FokI	FspI	GdII	HaeI	HaeII
HaeIII	HaeIV	HgaI	HgiEII	HhaI	Hin4I	HincII	HindIII
HinfI	HphI	KpnI	MaeIII	MboII	MluI	MmeI	MnlI
MscI	MseI	MslI	MspI	MspAII	MunI	MwoI	NciI
NcoI	NgoAV	NheI	NlaIII	NlaIV	NruI	NsiI	NspI
NspV	Pfl1108I	PleI	PshAI	PstI	PvuI	RcaI	RleAI
RsaI	Saci	Sali	Sapi	Sau96I	Sau3AI	Scal	ScrfI
SfaNI	SfcI	SimI	SmaI	SmlI	SnaBI	SpeI	SspI
StyI	TaiI	TagI	TaqII	TatI	TauI	TfiI	Thai
TseI	Tsp45I	Tsp509I	TspRI	Tth111II	UbaLI	VspI	XbaI

Enzymes that do not cut:

AatII	AloI	ApaI	AvrII	BaeI	BbsI	BbvCI	BmgI
BglI	Bpu10I	Bpu102I	BsbI	BseRI	BsmBI	BspEI	BstAPI
BstEII	BstXII	BstZ17I	Bsu36I	DraIII	DrdII	EagI	Eco47III
EcoNI	EcoO109I	FseI	HpaI	NarI	NdeI	NotI	PacI
PflMI	PinAI	PmeI	PmlI	Psp5II	PvuII	RsrII	SacII
SanDI	SbfI	SexAI	SfiI	Sgfi	SgrAI	SphI	SrfI
Sse8647I	StuI	SunI	SwaI	Tth111II	XcmI		

12-11-1998

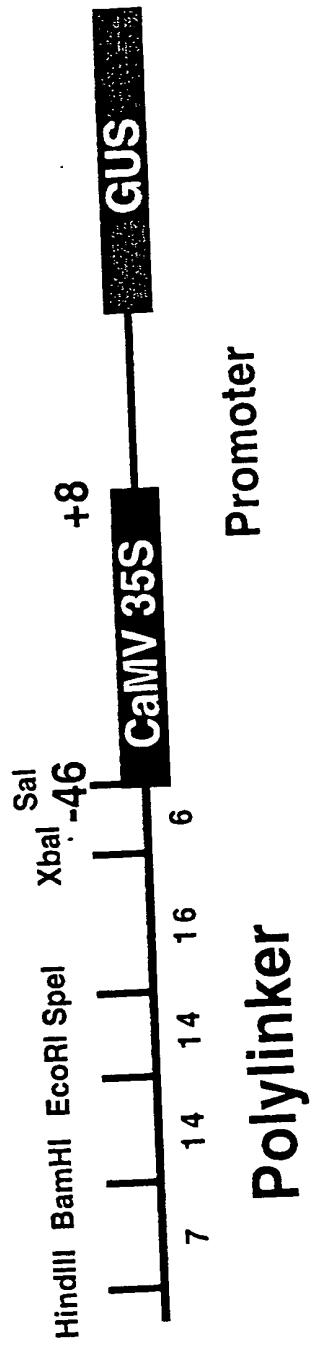
EP98121160.0

DRAW

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Fig. 2

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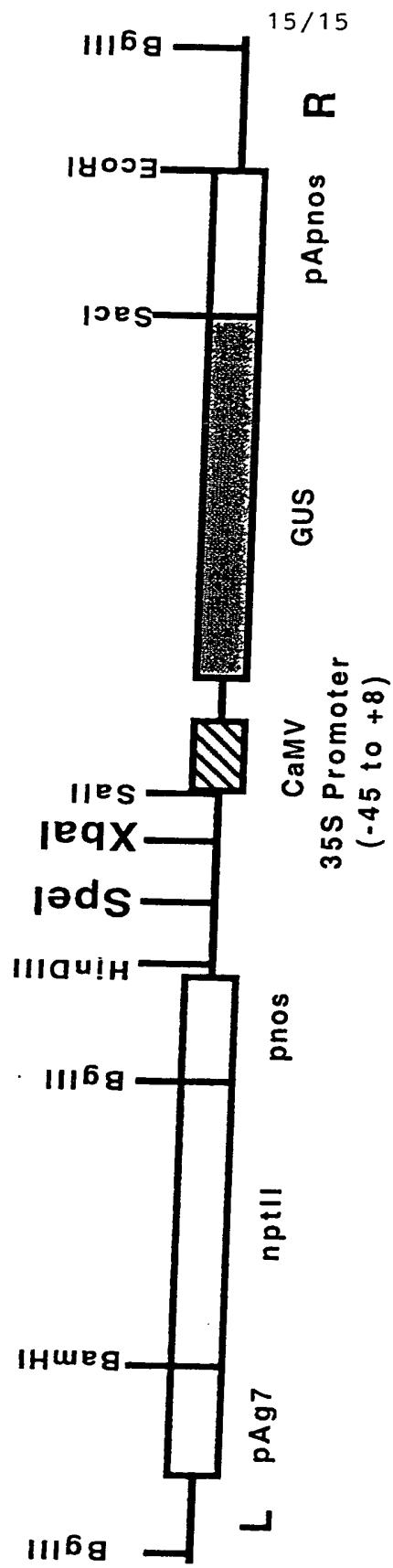
pGPTV-GUS-Kan

Fig. 3

